

SEQUENCE CHARACTERISTICS:
 LENGTH: 2808 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double
 Topology: linear
 MOLECULE TYPE: cDNA
 HYDROPHOBIC: NO
 ANTI SENSE: NO
 US 07 708 962 1

Query Match 1.98; Score 68.8; DB 1; Length 2808;

Best local Similarity 53.18; Pred. No. 1.2e-07;

Matches 170; Conservative 0; Mismatches 147; Indels 4; Gaps 1;

QY 1922 AGAAGGATTCGAATACAGTCTCTTCTTATATAAAGATGATGGCTAGGCT 1981
 DB 1440 AAGAGGATTCGAATACAGTCTCTTCTTATATAAAGATGATGGCTAGGCT 1999
 QY 1982 ATCTGGGAGTAAATACATCTTCTTCTTATATAAAGATGATGGCTAGGCT 2041
 DB 2030 GGTGAGTAAATACATCTTCTTCTTATATAAAGATGATGGCTAGGCT 2056
 QY 2042 TATCTGAGTAAATACATCTTCTTCTTATATAAAGATGATGGCTAGGCT 2101
 DB 2057 ACATAGAGTAAATACATCTTCTTCTTATATAAAGATGATGGCTAGGCT 2116
 QY 2162 ATTGGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 2161
 DB 2117 ATTGGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 2176
 QY 2162 TAAATTCGAAATACATCTTCTTCTTATATAAAGATGATGGCTAGGCT 2221
 DB 2177 GATCTTCGAAATACATCTTCTTCTTATATAAAGATGATGGCTAGGCT 2236
 QY 2222 TAAATTCGAAATACATCTTCTTCTTATATAAAGATGATGGCTAGGCT 2241
 DB 2247 AATAGAGTAAATACATCTTCTTCTTATATAAAGATGATGGCTAGGCT 2256

RESULT 14

US 08 106 494A 1

Sequence 1, Application US/08106494A

Patent No. 5457049

GENERAL INFORMATION:

APPLICANT: Antonio Giordano

TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN PRB2,

TITLE OF INVENTION: RELATED GENE PRODUCTS, AND DNA ENCODING

TITLE OF INVENTION: THEREFOR"

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Temple University of The Commonwealth

STREET: 406 University Services Building

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19122

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08-106-494A

FILING DATE: August 12, 1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mullins, J.G.

REGISTRATION NUMBER: 43,074

REFERENCE/DOCKET NUMBER: 6056-188

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5949

TELEX: No. 5457049e

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4249 base pairs

TYPE: nucleic acid

STRANDEDNESS: Single

TOPOLOGY: linear

US-08-106-494A-1

Query Match 1.98; Score 68.2; DB 1; Length 4249;

Best local Similarity 53.08; Pred. No. 1.8e-07;

Matches 170; Conservative 0; Mismatches 148; Indels 4; Gaps 1;

QY 1922 AGAAGGATTCGAATACATCTTCTTCTTATATAAAGATGATGGCTAGGCT 1981
 DB 2112 ATACAGGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 2171
 QY 1982 ATCTGGGAGTAAATACATCTTCTTCTTATATAAAGATGATGGCTAGGCT 2041
 DB 2372 CTGCGGATTCGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2428
 QY 2042 TCACTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 2101
 DB 2429 AATCTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 2488
 QY 2502 ATTGGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 2161
 DB 2489 ATTGGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 2548
 QY 2562 TTAATTCGAAATACATCTTCTTCTTATATAAAGATGATGGCTAGGCT 2621
 DB 2549 AGTCTTCGAAATACATCTTCTTCTTATATAAAGATGATGGCTAGGCT 2608
 QY 2222 TCAAGGCTTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 2242
 DB 2609 ATAGAGTAAATACATCTTCTTCTTATATAAAGATGATGGCTAGGCT 2629

RESULT 14

US-08-429-264-1

Sequence 1, Application US/08429264

Patent No. 5532440

GENERAL INFORMATION:

APPLICANT: Antonio Giordano

TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN

TITLE OF INVENTION: PRB2"

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seigel, Gonda, Lavorata & Monaco, P.C.

STREET: 1800 Two Penn Center Plaza

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08-429-264

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/106,493

FILING DATE: August 12, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, D.A.

REGISTRATION NUMBER: 40,480

REFERENCE/DOCKET NUMBER: 6056-188

1 CORRESPONDENT ADDRESS:
 2 ADDRESSEE: Campbell and Flores
 3 STREET: 4470 La Jolla Village Drive, Suite 700
 4 CITY: San Diego
 5 STATE: California
 6 COUNTRY: USA
 7 ZIP: 92122
 8 COMPUTER READABLE FORM:
 9 MEDIUM TYPE: Floppy disk
 10 COMPUTER: IBM PC compatible
 11 OPERATING SYSTEM: PC-DOS/MS-DOS
 12 SOFTWARE: Patent Release #1.0, Version #1.25
 13 CURRENT APPLICATION DATA:
 14 APPLICATION NUMBER: US/08/959,648
 15 FILING DATE:
 16 CLASSIFICATION:
 17 PRIOR APPLICATION DATA:
 18 APPLICATION NUMBER: US/08/128,673
 19 FILING DATE: 25-OCT-1994
 20 APPLICATION NUMBER: US/08/233,777
 21 FILING DATE: 19-MAY-1994
 22 PRIOR APPLICATION DATA:
 23 APPLICATION NUMBER: US/08/142,669
 24 FILING DATE: 25-OCT-1993
 25 ATTORNEY/AGENT INFORMATION:
 26 NAMES: Campbell, Cathryn A.
 27 REGISTRATION NUMBER: 41,815
 28 REFERENCE/DOCKET NUMBER: P-CJ 1192
 29 TELECOMMUNICATION INFORMATION:
 30 TELEPHONE: (619) 535-9001
 31 TELEFAX: (619) 535-8949
 32 INFORMATION FOR SEQ ID NO: 7:
 33 SEQUENCE CHARACTERISTICS:
 34 LENGTH: 2995 base pairs
 35 TYPE: nucleic acid
 36 STRANDEDNESS: single
 37 topology: linear
 38 FEATURE:
 39 NAME/KEY: CDS
 40 LOCATION: 139..2922
 41 US 08 959 648 7

Query Match 79.28; Score 2688; DB 2; Length 2995;
 Best Local Similarity 100.0%; Prod. No. 0;
 Matches 2688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GATTTTATGCTATTATTCAGAAAATTAAAGATATCATGATCATGTGACAGAGAGAGCTTGG 69
 DB 404 CATTTTAACTGATTAAGTCAAAATTAAGATATCATGATCATGTGACAGAGAGAGCTTGG 463
 QY 70 TTAATTTGGAGAAAGTTTCATCTGTGATGAGAGTATGGAGGTTATATTCAAAAGAAA 129
 DB 404 TTAATTTGGAGAAAGTTTCATCTGTGATGAGAGTATGGAGGTTATATTCAAAAGAAA 423
 QY 130 AAGAACTGCTGAGAAATGCTATTTATTCACAGAGTACCTACAGACATCTGCTTC 189
 DB 424 AAGAAATGCTGAGAAATGCTATTTATTCACAGAGTACCTACAGACATCTGCTTC 483
 QY 190 ACTTTTATGAGTACTAGAAAATAATAGAAATGAGTGTGATCAAAAATCTTTAACTTACTA 249
 DB 484 ACTTTTATGAGTACTAGAAAATAATAGAAATGAGTGTGATCAAAAATCTTTAACTTACTA 543
 QY 250 AAAAATAATGATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 309
 DB 544 AAAAATAATGATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 603
 QY 310 GATGATATGATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 369
 DB 604 GATGATATGATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 663
 QY 470 AAATGATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 429
 DB 664 AAATGATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 723

QY 430 ATCACAATTTTATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 489
 DB 724 ATCACAATTTTATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 783
 QY 490 TTTTCAATTAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 549
 DB 784 TTTTCAATTAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 843
 QY 550 AAATTAATTAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 609
 DB 844 AAATTAATTAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 903
 QY 610 GATGATATGATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 669
 DB 904 GATGATATGATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 963
 QY 670 GATGATATGATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 729
 DB 964 GATGATATGATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1023
 QY 730 TTTTCAATTAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 789
 DB 1024 TTTTCAATTAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 1083
 QY 790 AATCTTTCTAAACCATACGAGAAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 849
 DB 1084 AATCTTTCTAAACCATACGAGAAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1143
 QY 850 TTTTGGAGTAAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 909
 DB 1144 TTTTGGAGTAAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 1203
 QY 910 AATCTTTCTAAACCATACGAGAAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 969
 DB 1204 AATCTTTCTAAACCATACGAGAAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1263
 QY 970 AGGACTGTTTATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1029
 DB 1264 AGGACTGTTTATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1323
 QY 1030 CTTTTCAGAAAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 1089
 DB 1324 CTTTTCAGAAAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 1383
 QY 1090 CTGAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1149
 DB 1384 CTGAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1443
 QY 1150 CAGGCTGTTGTCGAAATTTGGAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTA 1209
 DB 1444 CAGGCTGTTGTCGAAATTTGGAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTA 1503
 QY 1210 CTAATTCGAAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 1269
 DB 1504 CTAATTCGAAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 1563
 QY 1270 CTTCTGAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1329
 DB 1564 CTTCTGAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1623
 QY 1330 GGCACATATACGATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 1389
 DB 1624 GGCACATATACGATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 1683
 QY 1390 TGGATTCGAAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 1449
 DB 1684 TGGATTCGAAATTAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 1743
 QY 1450 ATCAAGGAGAGGAGTAAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 1509
 DB 1744 ATCAAGGAGAGGAGTAAAGCTAAAGGGGAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 1803

[illegible][illegible]

Query Match 2.0% Score 68.23 DB 1: Length 3249;
Best Local Similarity 54.0% Pred. No. 1.6e 06;
Matches 170; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 1760 AAGAGCATTGAAATCTACCTCTCTTTTAAATGAGTATGAGTACCT 1819
DB 2412 ATAGAGAGAGAAAGCACTATTATCTTTTAAATGAGTATGAGTAC 2471
QY 1820 AICGCGGCTAAATATCTTTCGAGAACTTCTGAGCAATTAAGACA 1879
DB 2472 ATAGAGAGAGAAAGCACTATTATCTTTTAAATGAGTATGAGTAC 2471
QY 1880 TCACTGAGCTTTTTCAGCAAGCACTGAGCAATTAAGACA 1939
DB 2429 AAATCTGAGCTTTTTCAGCAAGCACTGAGCAATTAAGACA 2488
QY 1940 ATTTCAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 1999
DB 2489 ATCTGAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 2548
QY 2000 TTAATTCAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCA 2059
DB 2549 ATCTGAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 2608
QY 2060 TCAAGCTTTTTCAGCAATTAAGCAATTAAGCAATTAAGCAAT 2080
DB 2609 ATAGAGAGAGAAAGCACTATTATCTTTTAAATGAGTATGAGTAC 2679

RESULT 14
US-09-026-459a-30
Sequence 1: Application US/2001/02454
Patent No. 5542440
GENERAL INFORMATION:
APPLICANT: Antonio Giordano
TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN"
TITLE OF INVENTION: "PR2"
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
STREET: 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/2001/02454
FILING DATE:
CLASSIFICATION: 5.40
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,493
FILING DATE: August 12, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, D.A.
REGISTRATION NUMBER: 40,480
REFERENCE/BOOKET NUMBER: 6056-188 (11)
TELEPHONE: (215) 566-8483
TELEFAX: (215) 566-8483
TELEX: No. 5542440
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3249 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 70..3489

Query Match 2.0% Score 68.23 DB 1: Length 3249;
Best Local Similarity 54.0% Pred. No. 1.6e 06;
Matches 170; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 1760 AAGAGCATTGAAATCTACCTCTCTTTTAAATGAGTATGAGTACCT 1819
DB 2412 ATAGAGAGAGAAAGCACTATTATCTTTTAAATGAGTATGAGTAC 2471
QY 1820 AICGCGGCTAAATATCTTTCGAGAACTTCTGAGCAATTAAGACA 1879
DB 2472 ATAGAGAGAGAAAGCACTATTATCTTTTAAATGAGTATGAGTAC 2471
QY 1880 TCACTGAGCTTTTTCAGCAAGCACTGAGCAATTAAGACA 1939
DB 2429 AAATCTGAGCTTTTTCAGCAAGCACTGAGCAATTAAGACA 2488
QY 1940 ATTTCAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 1999
DB 2489 ATCTGAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 2548
QY 2000 TTAATTCAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCA 2059
DB 2549 ATCTGAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 2608
QY 2060 TCAAGCTTTTTCAGCAATTAAGCAATTAAGCAATTAAGCAAT 2080
DB 2609 ATAGAGAGAGAAAGCACTATTATCTTTTAAATGAGTATGAGTAC 2679

RESULT 15
US-09-026-459a-30
Sequence 1: Application US/2001/02454
Patent No. 5807681
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
APPLICANT: Baldi, Alphonso
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
TITLE OF INVENTION: OF CANCER
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,883
FILING DATE:
CLASSIFICATION: 4.55
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 40,480
REFERENCE/BOOKET NUMBER: 8421-13 US1
TELEPHONE: (215) 566-8483
TELEFAX: (215) 566-8483
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4854 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 70..3489

95 IleValLeuThrGlnProSerSerIleSerThrGluIleAsnSerAlaLeuValLeu 114
 116 AIAIAITIGACACAAACACACACAGTACGATGATGATGATGATGATGATGAT 486
 117 LysValSerIleThrIleLeuLeuAlaLysGlyGluValLeuGluMetGluAsp 134
 118 AAGTITITGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 546
 119 LeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerPro 154
 120 CIGGTCATITCATITCATITCATITCATITCATITCATITCATITCATITCAT 606
 121 ProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGlySerProArg 174
 122 GACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
 123 ThrProArgGlyGlnAspArgGlnAlaArgIleAlaLysGlnLeuGluAspThr 194
 124 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726
 125 ArgIleIleGluValLeuCysGlySerIleCysAsnIleAspGluValIleAsnVal 214
 126 AGAATITATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 786
 127 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeu 234
 128 IATITCAAAATITATGATGATGATGATGATGATGATGATGATGATGATGAT 846
 129 ProIleValGluAsnLeuSerIleAspTyrGluGluIleTyrLeuLysAsnLysAspLeu 254
 130 CGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 906
 131 AspAlaArgIleLeuPheLeuAspIleAspIleLeuGlnIleThrSerIleAspSerPhe 274
 132 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 966
 133 GlnThrIleArgThrProArgIleAsnLeuAspGluGluValValIleProPro 294
 134 GAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1026
 135 HisThrProValArgIleValMetAsnThrIleGlnIleGlnLeuMetMetIleLeuAsnSer 314
 136 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1086
 137 AlaserAspGlnProSerGlnAsnLeuIleSerTyrPheAsnAsnCysThrValIleAsnPro 334
 138 GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1146
 139 LysIleSerIleLeuLysAlaValLysAspIleGlyTyrIlePheLysGluLysPheAla 354
 140 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1206
 141 LysAlaValGlyGlnGlyLysValGluIleGlySerGlnArgTyrLysLeuGlyValArg 374
 142 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1266
 143 LeuIleTyrArgValMetGlnSerMetLeuLysSerGluGluGluArgLeuSerIleGln 394
 144 IATITACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1326
 145 AsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeu 414
 146 AATITACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1386
 147 GluValValMetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAsp 434
 148 GAGTITGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1446
 149 LeuSerPheThrIlePheLeuAsnValIleLeuAsnLeuLysAlaPheAspPheLysVal 454
 150 IATITACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1506
 151 IleGlnSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLysIleLeuGlu 474

1507 ATGGAAGTTTATCAAAAGACAAAGGCAATTCGACAAAGAAATGATAAATATTGAA 1566
 475 ArgCysGlnHisArgIleMetGluSerLeuAlaIlePheLeuSerAspSerProLeuLeuAsp 494
 1567 GATATGAAATATCAAAATATCAAAATATCAAAATATCAAAATATCAAAATATCAAA 1626
 495 LeuIleLysLeuSerLysAspArgGluGlyProThrAspHisLeuGluLysSerAlaCysPro 514
 1627 CTAAATTAACATCAAAAGGCAATTCGACAAAGAAATGATAAATATTGAAATATTG 1686
 515 LeuAsnLeuProLeuGlnAsnAsnIleThrAlaAlaAspMetTyrLeuSerProValArg 534
 1687 CTTAATTCCTTCGACAAATATCAAAATATCAAAATATCAAAATATCAAAATATTG 1746
 535 SerProLysLysLysSerThrThrArgValAsnSerThrAlaAsnAlaCysIleCys 554
 1747 TCTGCAAAATCAAAAGGCAATTCGACAAAGAAATGATAAATATTGACAAATGACAA 1806
 555 AlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyr 574
 1807 GCAACATGACCTTCACAAAGGCAATTCGACAAAGAAATGATAAATATTGACAAAT 1866
 575 LysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSer 594
 1867 AAAAAAGTATGCGTATGCGTATGCGTATGCGTATGCGTATGCGTATGCGTATGCGT 1926
 595 GlnHisProLeuLeuGlnHisIleIleThrPheLeuPheGlnHisThrLeuGluAsnGlu 614
 1927 GAAATCAAAATATCAAAATATCAAAATATCAAAATATCAAAATATCAAAATATT 1986
 615 TyrGluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIle 634
 1987 TATCAACATGATGACGACAGGCAATTCGACAAAGAAATGATAAATATTGACAAAT 2046
 635 CysLysValLysAsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeu 654
 2047 TCGAAAGTATGAAATATGAAATATGAAATATGAAATATGAAATATGAAATATT 2106
 655 ProHisAlaValIleGlnCysArgValLeuIleLysGluGluGlyLysSer 674
 2107 CTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2166
 675 IleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlyTyr 694
 2167 ATATATATATTCATACGATGATGATGATGATGATGATGATGATGATGATGAT 2226
 695 AlaserThrArgProProThrLeuSerProIleProHisIleProArgSerProTyrLys 714
 2227 GATATCAAAATATCAAAAGGCAATTCGACAAAGAAATGATAAATATTGAAAT 2286
 715 PheProSerSerProLeuArgIleThrGlyCysAsnIleGlyIleSerProGluLysSer 734
 2287 TTCTATATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2346
 735 ProTyrLysIleSerGlyLeuProThrProThrLysMetThrProArgSerArgIle 754
 2347 CCATATCAAAATATCAAAAGGCAATTCGACAAAGAAATGATAAATATTGAAAT 2406
 755 LeuValSerIleGlyGluSerPheLysThrSerGluLysPheGluLysIleAsnGluMet 774
 2407 TTATATATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2466
 775 ValCysAsnSerAspArgValIleLeuLysArgGlnAlaGluGlySerAsnProGlySer 794
 2467 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2526
 795 LeuValSerIleArgPheAsnThrLeuGlySerAspIleAlaAspGlySerGlyIleLeu 814
 2527 GCGAAATATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2586
 815 ProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMet 834

SEQUENCE CHARACTERISTICS:
 LENGTH: 4266 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2502
 SEQUENCE DESCRIPTION: SPQ ID No. 34.
 US-09-026-459a-39

Alignment Scores:
 Freq. No. Length: 3264
 Score: 4217.00 Matches: 821
 Percent Same: 100.00% Conserved: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.23% Indels: 0
 Gaps: 0

US-09-026-459a-39 (1-951) x US-09-469-522-34 (1-3266)

37 ValAspLeuAspGluMetSerPheThrPheThrGluLeuGlnIleLysAsnIleGlnIleSer 50
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RESULT 10

US-09-469-522-28

Sequence 28, Application 03/09469522

Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Hendrick, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

```
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: Arnold, White & Durkee
5 STREET: P.O. Box 4433
6 CITY: Houston
7 STATE: TX
8 COUNTRY: USA
9 ZIP: 77210-4433
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patent In Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/09/469,522
17 FILING DATE: 22-Dec-1999
18 CLASSIFICATION: <Unknown>
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 09/026,459
21 FILING DATE: <Unknown>
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Hibler, David W.
24 REGISTRATION NUMBER: 41,071
25 REFERENCE/JACKET NUMBER: 01XC:506
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: 512/418-3000
28 TELEFAX: 512/474-7577
29 INFORMATION FOR SEQ ID NO: 28:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 3455 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35 FEATURE:
36 NAME/KEY: CDS
37 LOCATION: 7..2691
38 SEQUENCE DESCRIPTION: SEQ ID NO: 28:
39 US-09-469-522-28
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Alignment Scores:

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Score: 4217.00 Matches: 821
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Job time : 150.122 secs

GenCore version 5.1.1.4
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Run on: January 16, 2003, 15:20:22 : Search time 94.55:55 Seconds
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16420.731 Million cell updates/sec

Title: US-09-026-459A 40

Perfect score: 4461
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Searched: 49868 seqs, 22294149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum hit seq length: 6
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Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	4353.8	96.9	4849	US-09-454-531-143	Sequence 143, Appl
4	4351.6	96.8	4554	US-09-469-522-50	Sequence 50, Appl
5	4247.34	93.8	4455	US-09-469-522-28	Sequence 28, Appl
6	4228	93.3	4323	US-09-469-522-38	Sequence 38, Appl
7	4225.4	93.2	4256	US-09-469-522-34	Sequence 34, Appl
8	4225.4	93.2	4323	US-09-469-522-32	Sequence 32, Appl
9	4225.4	93.2	4392	US-09-469-522-30	Sequence 30, Appl
10	4212	92.8	4218	US-09-469-522-3	Sequence 3, Appl
11	3109	89.8	4347	US-09-469-522-42	Sequence 42, Appl
12	4107	89.8	3113	US-09-469-522-36	Sequence 36, Appl
13	2996.4	86.6	3383	US-09-469-522-48	Sequence 48, Appl
14	2984.4	86.2	3377	US-09-469-522-46	Sequence 46, Appl
15	2827.4	81.7	3163	US-09-469-522-44	Sequence 44, Appl
16	2657.2	76.8	2995	US-09-860-211-7	Sequence 7, Appl
17	428	12.4	451	US-09-796-692-7740	Sequence 7740, Ap
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19	129	3.7	129	US-09-864-761-19910	Sequence 19910, A

20	104	3.0	304	10	US-09-464-824A-296	Sequence 296, App
21	68.8	2.0	3960	9	US-09-242-758-37	Sequence 37, Appl
22	59.4	1.7	324	9	US-09-796-692-2546	Sequence 2546, Ap
23	51	1.5	3747	10	US-09-770-657-1	Sequence 1, Appl
24	51	1.5	3747	12	US-10-025-626-2	Sequence 2, Appl
25	49.4	1.4	640681	10	US-09-790-988-1	Sequence 1, Appl
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35	45.8	1.3	431	10	US-09-960-352-5558	Sequence 5558, Ap
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43	44.2	1.3	1476	10	US-09-070-927A-749	Sequence 749, App
44	44.2	1.3	2000	9	US-09-938-842A-5166	Sequence 5166, Ap
45	44.2	1.3	3209	10	US-09-220-091-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-469-522-40
: Sequence 40, Application US-09469522
: Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji
Hu, Shi Xue
Benedict, William F.
Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOLBLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.40

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999

PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Hilbert, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UIX0:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 3461 base pairs
TYPE: nucleic acid

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QY 3241 GATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
1b 3241 GATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3300
QY 3301 GATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
1b 3301 GATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
QY 3361 GATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420
1b 3361 GATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420
QY 3421 GATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3461
1b 3421 GATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3461

RESULT 2

US-09-469-522-1
Sequence 1, Application US/09469522
Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Zhou, Yunli
Benedict, William F.

TITLE OF INVENTION: MODIFIED RETIN-BLASTOMA TUMOR SUPPRESSOR
PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210 4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09469,522
FILING DATE: 22 Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: Unknown

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: OTX-506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-8000
TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3555 base pairs

TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 7..2790

121 CGGAGGACCTGGCTTCTGTCACGCTTGGTTGAGTGAAGAACAGAGAAAGCTGATTTACT 180
121 CCGACGACCTGGCTTCTGTCACGCTTGGTTGAGTGAAGAACAGAGAAAGCTGATTTACT 180
141 GCATTAATGTCAGAAAATTAAGACATACAGACATGACAGACAGAGAGCTTGGTT 233
181 GCATTAATGTCAGAAAATTAAGACATACAGACATGACAGACAGAGAGCTTGGTT 240
244 ----- 233
241 GAAAAATTTTCATCTGTCGACATGAGGAGTTATTTCAAAAGAAAAAGGAAC 300
244 -----GGTGGACCTAGAGATGATGATTTACT 267
401 TGGGAAATCTGATCTGATGAGGAGTTGACCTAGGTCATGCTGCTTACT 360
268 GACCTATAGAAAAATACAAATCAGTGTCCATAAATCTTTAACTTAAAGAAAT 327
361 GATTAATAGAAAAATACAAATCAGTGTCCATAAATCTTTAACTTAAAGAAAT 420
428 GATTAATAGAAAAATACAAATCAGTGTCCATAAATCTTTAACTTAAAGAAAT 387
421 GATTAATAGAAAAATACAAATCAGTGTCCATAAATCTTTAACTTAAAGAAAT 480
388 TTTGATCTTCTGAGTAAATGGAAGACATGAGTATATATTTGACACAAAGCAGC 447
481 TTTGATCTTCTGAGTAAATGGAAGACATGAGTATATATTTGACACAAAGCAGC 540
448 AGTTCGATATCTGAGTAAATGGAAGACATGAGTATATATTTGACACAAAGCAGC 507
541 AGTTCGATATCTGAGTAAATGGAAGACATGAGTATATATTTGACACAAAGCAGC 600
508 TTTGATCTTCTGAGTAAATGGAAGACATGAGTATATATTTGACACAAAGCAGC 567
601 TTTGATCTTCTGAGTAAATGGAAGACATGAGTATATATTTGACACAAAGCAGC 660
568 ATGATCTTCTGAGTAAATGGAAGACATGAGTATATATTTGACACAAAGCAGC 627
661 ATGATCTTCTGAGTAAATGGAAGACATGAGTATATATTTGACACAAAGCAGC 720
628 TATAAATAGCTGTATACCATTAATGATGATGATGATGATGATGATGATGATGAT 687
721 TATAAATAGCTGTATACCATTAATGATGATGATGATGATGATGATGATGATGAT 780
688 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 747
741 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
748 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807
841 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
808 TTTGATCTTCTGAGTAAATGGAAGACATGAGTATATATTTGACACAAAGCAGC 867
901 TTTGATCTTCTGAGTAAATGGAAGACATGAGTATATATTTGACACAAAGCAGC 960
868 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 927
961 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
928 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 987
1021 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
988 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1047
1081 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
1048 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1107
1141 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
1108 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1167

1201 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
1168 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1227
1261 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1420
1228 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1287
1321 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
1288 TCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1347
1381 TCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
1348 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1407
1441 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1408 AGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1467
1501 AGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
1468 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1527
1561 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
1528 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1587
1621 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
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1681 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
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1741 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
1708 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1767
1801 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
1768 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1827
1861 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
1828 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1887
1921 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
1888 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1947
1981 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
1948 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2007
2041 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
2008 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2067
2101 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
2068 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2127
2161 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
2128 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2187
2221 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
2188 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2247

1984 CTTAAATTCAGAAATCACTGTAACAGATATACAGATATGCTGCTCAGGACACA 2043
QY TTTAAATCTTTTATTAAGAAAGAGATGATGATGATGATGATGATGATGATGAT 2187
DB TTTAAATCTTTTATTAAGAAAGAGATGATGATGATGATGATGATGATGATGAT 2193
QY CTTTCACTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2247
DB CTTTCACTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2163
QY TTTTCACTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2307
DB TTTTCACTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2223
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2367
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2283
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2427
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2343
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2487
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2403
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2547
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2463
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2607
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2523
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2667
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2583
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2727
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2643
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2787
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2703
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2847
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2763
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2907
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2823
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2967
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2883
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3027
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2943
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3087
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3003
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3147
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3063
QY ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3207
DB ATCTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3123

QY 3208 AAAATGCGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4257
DB 3124 AAAATGCGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3183
QY 3268 TTACTATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4327
DB 3184 TTACTATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3243
QY 3328 AAAAGCTGGAGCAATATATATATATATATATATATATATATATATATATAT 3387
DB 3244 AAAAGCTGGAGCAATATATATATATATATATATATATATATATATATATAT 3303
QY 3388 CTTTCACTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3447
DB 3304 CTTTCACTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3363
QY 3448 GGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3461
DB 3364 GGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3377

RESULT 15
US-09-469-522-44
: Sequence 44, Application US/09469522
: Patent No. US20020151461A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: Hu, Shi-Xue
: Benedict, William F.
: Zhou, Yunli
: TITLE OF INVENTION: MODIFIED REINCHLASTOMA TUMOR SUPPRESSOR
: PROTEINS
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESS: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/469,522
: FILING DATE: 22-Dec-1999
: CLASSIFICATION: <Unknown>
: FILED APPLICATION DATA:
: APPLICATION NUMBER: 09/026,459
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Hibler, David W.
: REGISTRATION NUMBER: 41,071
: REFERENCE/DOCKET NUMBER: DIX:506
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512/418-3000
: TELEFAX: 512/474-7577
: INFORMATION FOR SEQ ID NO. 44:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3161 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 7..2397
: SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-469-522-44

Query Match 81.7%, Score 2827.4, DB 10, Length 3161.

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QY	617	TCAAGAAATATATAAANAGTCTTTATAGCAATTAATGGTTACGTGCAACAAACAGGCG	676			
DB	417	TTATGCAACAGCTTCACTTAATGTTATACCCATTAATGGTTACGTGCAACAAACAGGCG	376			
QY	677	GAGGTCACAAAG	736			
DB	477	GAGGTCACAAAG	436			
QY	737	AAAGCTTCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	796			
DB	437	AAAGCTTCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	496			
QY	797	ATTATATAGCTTTTATTAATTTCTTGGATTTGATTTATTTATTTATTTATTTATTTAT	856			
DB	497	ATTATATAGCTTTTATTAATTTCTTGGATTTGATTTATTTATTTATTTATTTATTTAT	556			
QY	857	AAAAATTTCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	916			
DB	557	AAAAATTTCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	616			
QY	917	TATTTGCAATCAGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	976			
DB	617	TATTTGCAATCAGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	676			
QY	977	GAAAG	1036			
DB	677	GAAAG	736			
QY	1037	TATGCAATCAGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	1096			
DB	737	TATGCAATCAGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	796			
QY	1097	AAATTTCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	1156			
DB	797	AAATTTCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	856			
QY	1157	TATTTGAAG	1216			
DB	857	TATTTGAAG	916			
QY	1217	GAAAG	1276			
DB	917	GAAAG	976			
QY	1277	TATGCAATCAGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	1336			
DB	977	TATGCAATCAGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	1036			
QY	1337	AAATTTCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	1396			
DB	1037	AAATTTCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	1096			
QY	1397	TATTTGAAG	1456			
DB	1097	TATTTGAAG	1156			
QY	1457	TATGCAATCAGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	1516			
DB	1157	TATGCAATCAGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	1216			
QY	1517	TTATTTGAAG	1576			
DB	1217	TTATTTGAAG	1276			
QY	1577	ATTTGAAG	1636			
DB	1277	ATTTGAAG	1336			
QY	1637	AAATTTGAAG	1696			

DB	1337	AAATTTGAAG	1396			
QY	1697	CTCTGCAAGAAATTAATCAGACTGCAAGAGATATGATGATGATGATGATGATGATGATGAT	1756			
DB	1397	CTCTGCAAGAAATTAATCAGACTGCAAGAGATATGATGATGATGATGATGATGATGATGAT	1456			
QY	1757	AAAAAGGTTCAACTACGGCTGCTAAATTTCTACATGCAAAATGCAAGAGACACAAAGACAG	1816			
DB	1457	AAAAAGGTTCAACTACGGCTGCTAAATTTCTACATGCAAAATGCAAGAGACACAAAGACAG	1516			
QY	1817	CTTTGCAAG	1876			
DB	1517	CTTTGCAAG	1576			
QY	1877	ATGGCTAGCTATGCTGGCTTAAATACACTTTGTAAGAGCTGCTGCTGCAAGAGAGAGAG	1936			
DB	1577	ATGGCTAGCTATGCTGGCTTAAATACACTTTGTAAGAGCTGCTGCTGCAAGAGAGAGAG	1636			
QY	1937	AAATTAAGAAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1996			
DB	1637	AAATTAAGAAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1696			
QY	1997	TGAG	2056			
DB	1697	TGAG	1756			
QY	2057	AGAAATATAGAGCTTAAATTTAAATATGATGATGATGATGATGATGATGATGATGATGAT	2116			
DB	1757	AGAAATATAGAGCTTAAATTTAAATATGATGATGATGATGATGATGATGATGATGATGAT	1816			
QY	2117	TTCAG	2176			
DB	1817	TTCAG	1876			
QY	2177	TCTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2236			
DB	1877	TCTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1936			
QY	2237	GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2296			
DB	1937	GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1996			
QY	2297	CAGCTTGAAG	2356			
DB	1997	CAGCTTGAAG	2056			
QY	2357	TTTCAG	2416			
DB	2057	TTTCAG	2116			
QY	2417	TTGGTGAATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2476			
DB	2117	TTGGTGAATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2176			
QY	2477	GCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2536			
DB	2177	GCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2236			
QY	2537	TAGGCTTTGATATGAG	2596			
DB	2237	TAGGCTTTGATATGAG	2296			
QY	2597	CCAAATTTTCAAG	2656			
DB	2297	CCAAATTTTCAAG	2356			
QY	2657	AAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2716			
DB	2357	AAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2416			
QY	2717	GTTGAG	2776			
DB	2417	GTTGAG	2476			

QY	2777	CAAGGCTTCGCTTAAAGCTACACATTTAAATCTCTCAGCTCTCTTTTCTGGCATATAAAATGCTG	28383
DB	2477	CAAGCTTTCTTTTATAGCTGTAATTAATATCTTCAAGCTCTTTTCTGGATATAAATATGCTG	2536
QY	2837	TACATCTAAATCTCTTGGGTCATCTCTTAAGCCACTTGAATCTCTAGTCACTCTTAATTATA	2896
DB	2537	CAATGCTAAATCTTTTGGGTCATCTCTTAAGCCACTTGAATCTCTAGTCACTCTTAATTATA	2596
QY	2897	CAAGATTGAATATCTTCTGCTTAATCTCTGCCATTTTAAANAATTTGACAGCAATCTTCTCTCT	2956
DB	2597	CAATATAGAATACTCTTCTGCTTAAATCTCTGCCATTTTAAANAATTTGACAGCAATCTTCTCTCT	2656
QY	2957	TTCCTAAGTAAATATCTCTGCTCTTAAATCTCTGCCATTTTAAANAATTTGACAGCAATCTTCTCTCT	3016
DB	2657	TTCCTAAGTAAATATCTCTGCTCTTAAATCTCTGCCATTTTAAANAATTTGACAGCAATCTTCTCTCT	2716
QY	3017	GATAAATCTAGGCTCTCTGACTACTCTTGGCTCTCTCTTCTAGCATATAGCTGATCTTTGCT	3076
DB	2717	GAATAAATAGGCTCTCTGACTACTCTTGGCTCTCTCTTCTAGCATATAGCTGATCTTTGCT	2776
QY	3077	CTTCTTTTTTAAATTTATATATATATATTTTTTTTAAATTTAGCATGACACCTTAGAATAAT	3136
DB	2777	CTTCTTTTTTAAATTTATATATATATATTTTTTTTAAATTTAGCATGACACCTTAGAATAAT	2836
QY	3137	GTCGCTATCTATCTCTTCTGCTAAATCTGATCTGACTTGGCCATCTACCAAAATTTATCTCTG	3196
DB	2837	GTCGCTATCTATCTCTGCTAAATCTGATCTGACTTGGCCATCTACCAAAATTTATCTCTG	2896
QY	3197	AAGCTCTCTCTGCTAAATCTGATCTGACTGAAATTTAGAAAAAATTTACTAAATTTACACAT	3256
DB	2897	AAGCTCTCTCTGCTAAATCTGATCTGACTGAAATTTAGAAAAAATTTACTAAATTTACACAT	2956
QY	3257	TAGATTTTATTTTATCTATCTGGAATCTGATATCTGCTGCTCTGCTTTTAAATAAATTTGCT	3316
DB	2957	TAGATTTTATTTTATCTATCTGGAATCTGATATCTGCTGCTCTGCTTTTAAATAAATTTGCT	3016
QY	3317	TTTAAATTAATTAAGCTCTGGAAGCAAGTATTAAGCATATGATCTACTATCATCTACTACAAA	3376
DB	3017	TTTAAATTAATTAAGCTCTGGAAGCAAGTATTAAGCATATGATCTACTATCATCTACTACAAA	3076
QY	3377	CAGATTTTCACTCAGAACTGTAAGAAGCACTTACGATATTTTCTCTCTCATCTCAACTATG	3436
DB	4077	CAGATTTTCACTCAGAACTGTAAGAAGCACTTACGATATTTTCTCTCTCATCTCAACTATG	3136
QY	4437	TTTTTAATGAGGATTTATTTGATAT	3461
DB	3137	TTTTTAAATGAGGATTTATTTGATAT	3161

Search completed: January 18, 2003, 04:28:20
 Job time : 131.552 secs

GenCore version 5.1.3
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QM protein - nucleotide search, using frame-plus-p2n model
Run on: January 18, 2003 04:41:54 : Search time 65.4803 Seconds
(without alignments)
6107.852 Million cell updates/sec

Title: US-09-026-459A-41

Perfect score: 46.31
Sequence: 1 MPKTPKTAATAAAAAAEP.....TRMKKKNMSDEISNKKK 897

Scoring table:

Match 10.0, Xgapext 9.5
Xgapop 10.0, Ygapext 9.5
Egapop 6.0, Fgapext 7.0
Egapop 6.0, Delext 7.0

Searches: 39868 seqs, 22944149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOCAL=0 -LOCALEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-biosum62
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Database : Published Applications_NA:

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2: /seq2_6/ptdata/1/pubpna/pet_NEW_PUB seq:
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8: /seq2_6/ptdata/1/pubpna/us08_PURCOMB seq:
9: /seq2_6/ptdata/1/pubpna/us09_NPW_PUB seq:
10: /seq2_6/ptdata/1/pubpna/us09_PURCOMB seq:
11: /seq2_6/ptdata/1/pubpna/us10_NEW_PUB seq:
12: /seq2_6/ptdata/1/pubpna/us10_PURCOMB seq:
13: /seq2_6/ptdata/1/pubpna/us06_NEW_PUB seq:
14: /seq2_6/ptdata/1/pubpna/us06_PURCOMB seq:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46.31	100.0	3461	10	US-09-469-522-40 Sequence 40, Appl
2	46.05	99.4	3555	10	US-09-469-522-18 Sequence 1, Appl
3	46.05	99.4	4839	9	US-09-954-531-143 Sequence 143, App
4	45.95	99.2	2995	10	US-09-860-211-7 Sequence 7, Appl

5	45.95	99.2	3554	10	US-09-469-522-50 Sequence 50, Appl
6	44.17	95.4	3455	10	US-09-469-522-28 Sequence 28, Appl
7	43.49	93.9	3323	10	US-09-469-522-38 Sequence 38, Appl
8	43.07	93.0	3392	10	US-09-469-522-40 Sequence 40, Appl
9	42.63	92.1	3377	10	US-09-469-522-46 Sequence 46, Appl
10	42.56	91.9	3383	10	US-09-469-522-48 Sequence 48, Appl
11	42.40	91.6	3347	10	US-09-469-522-42 Sequence 42, Appl
12	42.19	91.1	3323	10	US-09-469-522-32 Sequence 32, Appl
13	42.17	91.1	3265	10	US-09-469-522-34 Sequence 34, Appl
14	41.92	90.5	4218	10	US-09-469-522-3 Sequence 3, Appl
15	40.17	86.7	3113	10	US-09-469-522-46 Sequence 46, Appl
16	39.12	84.5	3161	10	US-09-469-522-44 Sequence 44, Appl
17	39.12	84.5	3161	10	US-09-469-522-44 Sequence 44, Appl
18	31.6	11.2	3747	10	US-09-725-657-1 Sequence 1, Appl
19	31.6	11.2	3747	10	US-10-025-657-2 Sequence 2, Appl
20	37.4	8.1	3209	10	US-09-920-691-4 Sequence 4, Appl
21	34.3	5.2	411	10	US-09-864-761-1141 Sequence 1141, Ap
22	218	4.7	129	10	US-09-864-761-19910 Sequence 19910, A
23	177.5	3.8	304	10	US-09-964-824A-276 Sequence 296, App
24	162.5	3.5	10096	10	US-09-960-253-163 Sequence 163, App
25	159.5	3.4	3624	9	US-10-108-605-216 Sequence 216, App
26	157.5	3.4	10198	10	US-09-864-864-292 Sequence 292, App
27	157.5	3.4	10211	10	US-09-954-456-1153 Sequence 1153, Ap
28	157.5	3.4	10211	10	US-09-967-768A-186 Sequence 186, App
29	156	3.4	6773	10	US-09-864-864-336 Sequence 336, App
30	151	3.3	5864	10	US-09-864-864-305 Sequence 305, App
31	147	3.2	4302	10	US-09-801-368-59 Sequence 59, Appl
32	146.5	3.2	8493	9	US-10-071-766-51 Sequence 51, Appl
33	145.5	3.1	224	9	US-09-796-692-2546 Sequence 2546, Ap
34	143	3.1	2526	9	US-09-938-842A-1242 Sequence 1242, Ap
35	141.5	3.0	9274	10	US-09-885-535-3 Sequence 3, Appl
36	141	3.0	4754	10	US-09-982-091A-1 Sequence 1, Appl
37	138	3.0	2637	10	US-09-815-242-686a Sequence 859, Ap
38	137.5	3.0	8473	10	US-09-851-682A-2 Sequence 2, Appl
39	137	3.0	1300	10	US-09-033-253-135 Sequence 135, App
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42	136	2.9	7792	12	US-10-044-090-359 Sequence 359, App
43	129	2.8	6504	10	US-09-801-368-55 Sequence 55, Appl
44	125.5	2.7	2988	10	US-09-815-242-4196 Sequence 4196, Ap
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ALIGNMENTS

RESULT 1
US-09-469-522-40
Sequence 40, Application US-09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOLASUMA TUMOR SUPPRESSOR

NUMBER OF SEQUENCES: 51

COMPRESS-NUCLEO ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/469,522

FILING DATE: 22-DEC-1999

CLASSIFICATION: <Unknown>

100


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DB 1816 GAGTAAATACACTTGTGAGAGGCTTCTGTGAGAGCAAGCAAGCAAGCAAGCAAGCAAG 1875
QY 618 TrpThrLeuPheGluHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 669
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RESULT 11

US-09-469-522-42
 : Sequence 42, Application US/09469522
 : Patent No. US20020151461A1
 : GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji
 Hu, Shi-Xue
 Benedict, William F.

Zhou, Yunli
 TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
 PROTEINS
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210-4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/046,459
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hibler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UTXC:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3347 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2583
 SEQUENCE DESCRIPTION: SEQ ID NO: 42:
 US-09-469-522-42

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 Best Local Similarity: 92.43% Mismatches: 19
 Query Match: 91.56% Indels: 38
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 QY 41 AspLeuProLeuValArgLeuGluPheGluGluGluGluGluGluGluGluGluGlu 60
 DB 127 CACTTGTCT 186
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 RESULT 32
 US 09 459 522 32
 Sequence 32: Application US/09459522
 Patent No: 200201341A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Hong-Ju
 Hu, Shi-Xue
 Zeng, Yuli
 TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
 PROTEINS
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210-4433
 COMPUTER PROGRAM FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patented software #10, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 09/459,522
 FILING DATE: 22-Dec-1999
 CLASSIFICATION: Unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: Unknown
 ATTORNEY/AGENT INFORMATION:
 NAME: Hibler, David W.
 REGISTRATION NUMBER: 41 071
 REFERENCE/DOCKET NUMBER: UTXC-506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 323 base pairs
 TYPE: nucleic acid
 STRANDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2559
 SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 US 09 459 522 32

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 Best Local Similarity: 96.83% Mismatches: 8
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 QY 205 LysGluProTyrLysThrAlaValIleProIleAspGlySerProArgThrProArgArg 224
 DB 481 AAAAATCATATAAAATAGTGTAT 540
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 DB 601 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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 DB 901 AAT 960
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 1141 GAAAGGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1200
 445 LeuLeuAsuAsuAsuGluGluGluGluGluGluGluGluGluGluGluGluGlu 464
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 1321 TGGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1380
 505 IleLysAlaGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 524
 1381 ATCAAAAGAAAGGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1440
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 RESULT 13
 US-09-459-522-34
 : Sequence 34, Application US/09459522
 : Patent No. US20020151461A1
 : GENERAL INFORMATION:
 : APPLICANT: Xu, Hong-Ji
 : Hu, Shi Xue
 : Benedict, William F.
 : Zhou, Yunli
 : TITLE OF INVENTION: MODIFIED RETIN-BLASTOMA TUMOR SUPPRESSOR
 : PROTEINS
 : NUMBER OF SEQUENCES: 51
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: AFGOLD, White & Burke
 : STREET: P.O. Box 4433
 : CITY: Houston
 : STATE: TX
 : COUNTRY: USA
 : ZIP: 77210-4433
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM pc compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.40
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09459522
 : FILING DATE: 22-Dec-1999
 : CLASSIFICATION: Unknown
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 09/026,459
 : FILING DATE: Unknown
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Hilder, David W.
 : REGISTRATION NUMBER: 41,071
 : REFERENCE/PACKET NUMBER: US/09459522
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 512/418-3000
 : TELEFAX: 512/474-7577
 : INFORMATION FOR SEQ ID NO: 34:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 4266 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 7..2502

REGISTRATION NUMBER: 41,071
REFERENCE/WORKET NUMBER: HIXC:506

TELEPHONE: 512/418 4000

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cm nucleic nucleic search, using sw model

Run on: January 16, 2003, 15:29:22 : Search time 91.4372 Seconds
(without alignments)
16820.741 Million cell updates/sec

Filter: US-09-026-459A 42

Perfect score: 3447

Sequence: 1 CGCGTCATGCGGCGCAAAAC.....AAATGAGSATTATGATACT 3347

Scoring table: IDENTITY NIK

Gapop 10.0 , Gapext 1.0

Sequences: 49808 seqs, 22294149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match OK

Maximum Match 100%

Listing first 45 summaries

- Database: Published Applications NA:
- 1: /com2_6/ptdata/1/pubpna/US07_PUBCOMB.seq
 - 2: /com2_6/ptdata/1/pubpna/US07_NEW_PUB.seq
 - 3: /com2_6/ptdata/1/pubpna/US06_NEW_PUB.seq
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 - 13: /com2_6/ptdata/1/pubpna/US10_NEW_PUB.seq
 - 14: /com2_6/ptdata/1/pubpna/US10_PUBCOMB.seq

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3447	100.0	3447	10	US-09-469-522-42 Sequence 42, Appl
2	3126.8	94.4	3554	10	US-09-469-522-50 Sequence 50, Appl
3	3126.8	94.4	3555	10	US-09-469-522-51 Sequence 51, Appl
4	3126.8	94.4	4839	9	US-09-954-531-143 Sequence 143, Appl
5	4111	92.9	3377	10	US-09-469-522-46 Sequence 46, Appl
6	4109	92.9	3461	10	US-09-469-522-40 Sequence 40, Appl
7	4066.2	91.6	3323	10	US-09-469-522-38 Sequence 38, Appl
8	4019.8	90.2	3455	10	US-09-469-522-28 Sequence 28, Appl
9	4006	89.8	4113	10	US-09-469-522-46 Sequence 36, Appl
10	4006	89.8	3216	10	US-09-469-522-34 Sequence 34, Appl
11	4006	89.8	3329	10	US-09-469-522-44 Sequence 44, Appl
12	4006	89.8	3329	10	US-09-469-522-32 Sequence 32, Appl
13	4006	89.8	3392	10	US-09-469-522-40 Sequence 30, Appl
14	2965	86.6	3161	10	US-09-469-522-44 Sequence 44, Appl
15	2911.4	87.0	3383	10	US-09-469-522-48 Sequence 48, Appl
16	2429.2	72.6	2995	10	US-09-860-211-7 Sequence 7, Appl
17	428	12.8	451	9	US-09-796-692-7740 Sequence 7740, Ap
18	142.2	4.2	411	10	US-09-864-761-3141 Sequence 3141, Ap
19	129	3.9	129	10	US-09-864-761-1910 Sequence 1910, A

20	104	3.1	304	10	US-09-964-824A-296 Sequence 296, Ap
21	68.8	2.1	396	9	US-09-292-798-37 Sequence 37, Appl
22	59.4	1.8	324	9	US-09-796-692-2546 Sequence 2546, Ap
23	51	1.5	3747	10	US-09-770-657-1 Sequence 1, Appl
24	51	1.5	3747	12	US-10-925-676-2 Sequence 2, Appl
c 25	49.4	1.5	640681	10	US-09-790-988-1 Sequence 1, Appl
26	48.8	1.5	335913	9	US-09-754-854A-2 Sequence 2, Appl
27	48.8	1.5	335913	9	US-09-754-854A-3 Sequence 3, Appl
c 28	48.4	1.4	419	10	US-09-969-373-442 Sequence 342, Ap
c 29	48.4	1.4	419	10	US-09-969-373-443 Sequence 343, Ap
c 30	48.4	1.4	513509	9	US-09-754-854A-4 Sequence 4, Appl
c 31	47.8	1.4	424	10	US-09-960-452-11218 Sequence 11218, A
c 32	47.6	1.4	411	10	US-09-960-452-14521 Sequence 14521, A
33	47	1.4	393	10	US-09-960-452-4582 Sequence 4582, Ap
c 34	46.2	1.4	302250	10	US-09-962-832-154 Sequence 154, Appl
c 35	46	1.4	2000	9	US-09-938-842A-3014 Sequence 3014, Ap
36	45.8	1.4	431	10	US-09-960-452-5558 Sequence 5558, Ap
37	45.6	1.4	419	10	US-09-960-452-11234 Sequence 11234, A
38	45.4	1.4	516	10	US-09-960-452-5785 Sequence 5785, Ap
c 39	45.2	1.4	640681	10	US-09-790-988-1 Sequence 1, Appl
c 40	44.6	1.3	555	10	US-09-864-761-12458 Sequence 12458, A
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c 44	44.4	1.3	2000	9	US-09-938-842A-4050 Sequence 4050, Ap
c 45	44.2	1.3	1376	10	US-09-070-927A-749 Sequence 749, Appl

ALIGNMENTS

RESULT 1

US-09-469-522-42

: Sequence 42, Application US/09469522

: Patent No. US20020151461A1

: GENERAL INFORMATION:

: APPLICANT: Xu, Hong-Ji

: Inventor: Xu, Hong-Ji

: Beneficiary: William F.

: Zhou, Yunli

: TITLE: INVENTION: MUTATED FLUORINOLANES: MAJUM & SUPPRESSOR

: PROTEINS

: NUMBER OF SEQUENCES: 51

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Arnold, White & Burke

: STREET: P.O. Box 4433

: CITY: Houston

: STATE: TX

: COUNTRY: USA

: ZIP: 77210-4433

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: OPERATING SYSTEM: IBM PC compatible

: SOFTWARE: Patent In Release #1.0, Version #1.40

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/469,522

: FILING DATE: 22-Dec-1999

: CLASSIFICATION: UNKNOWN

: PRIORITY APPLICATION DATA:

: APPLICATION NUMBER: 09/026,459

: FILING DATE: UNKNOWN

: ATTORNEY/AGENT INFORMATION:

: NAME: Hilder, David W.

: REGISTRATION NUMBER: 41,071

: REFERENCE/DOCKET NUMBER: UIX-506

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 512/418-4000

: TELEFAX: 512/474-7577

: INFORMATION FOR SEQ ID NO. 42:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 3347 base pairs

: TYPE: nucleic acid

601 AAAATTTTAACTTN'TAAMAAATAATGATACCAATACCAAGTTGATAAATGCTAATGCTCA 360
274 GATTAATTAATCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 310
603 AGA'TGTCAGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 420
611 GATTAATTTTAACTTN'TAAMAAATAATGATACCAATACCAAGTTGATAAATGCTAATGCTCA 366
621 GAA'TTAAATTAATCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 480
627 GATTAATTTTAACTTN'TAAMAAATAATGATACCAATACCAAGTTGATAAATGCTAATGCTCA 426
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QY 1327 ACAGATTTTCTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1386
DB 1331 ACAGATTTTCTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
QY 1387 AAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1446
DB 1501 AAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1447 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1506
DB 1561 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520
QY 1507 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1566
DB 1621 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1567 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1626
DB 1681 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
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DB 1741 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
QY 1687 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1746
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DB 1861 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
QY 1807 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1866
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QY 1867 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1926
DB 1981 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
QY 1927 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1986
DB 2041 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
QY 1987 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2046
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DB 2161 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
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DB 2221 TTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
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962	TT	
975	ATTTTAAATTCAGTAAGTCATTAACCTTCTGAAATAAATCTGATTTCTTAAATTTAAATAATGCG	834
	TT	
1021	ATACAGCAATTCAAAATCAAGCTATATCTGAAAATCAGTGAAGGATATATAGCATACATCTTTAAA	1080
1022	ATAGTCGAATCTCAAAAAGAAAGTATATCTGAAAATCTGAAGGATATATAGCATCTTTAAA	894
1081	GATAAATTTCTTAAAGTCTGGGACATATGCTTCTGAAAATCTGAAGGATATATAGCATCTTTAAA	1140
895	GATAAATTTCTTAAAGGCTCTGGGACATATGCTTCTGAAAATCTGAAGGATATATAGCATCTTTAAA	954
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955	CTTGGAAGTTCTGCTTATTTATGATTAATGCAATTCATGCTTTAAATCTGAAGGATATATAGCATCTTTAAA	1014
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1501	CTTTTATTTATCTTATTTAAATTAATCAAGGATATATAGCATCTTTAAATCTGAAGGATATATAGCATCTTTAAA	1560
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1681	CTGCTGGCTCTTCAAGCTTCTGAAAATCTGAAGGATATATAGCATCTTTAAATCTGAAGGATATATAGCATCTTTAAA	1740
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1615	CTGCTGGCTCTTCAAGCTTCTGAAAATCTGAAGGATATATAGCATCTTTAAATCTGAAGGATATATAGCATCTTTAAA	1674
1861	CTGCTGGCTCTTCAAGCTTCTGAAAATCTGAAGGATATATAGCATCTTTAAATCTGAAGGATATATAGCATCTTTAAA	1920
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1921	CTGCTGGCTCTTCAAGCTTCTGAAAATCTGAAGGATATATAGCATCTTTAAATCTGAAGGATATATAGCATCTTTAAA	1980
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2041	CTGCTGGCTCTTCAAGCTTCTGAAAATCTGAAGGATATATAGCATCTTTAAATCTGAAGGATATATAGCATCTTTAAA	2100

Db	1855	GAATATGATCTATTATA-TATTTCTATAACTGAGTGTCTTCATGACAGAACTGAAAAAATAAT	1914
QY	2101	ATTFTGCAGATATGCTTCCATCAGAGCGGCGTACCTTGTTCACCAATAGCTCAATATCTGCA	2160
Db	1915	ATTTTGCAGTATGCTTCACAGAGCGGCGTACCTTGTTCACCAATAGCTCAATATCTGCA	1974
QY	2161	AGCGCTTACAAAGTTGCTATCTTACAGCTTACGATCTGAGAGGAAATATATATATTCTTA	2220
Db	1975	AGCGCTTACAAAGTTGCTATCTTACAGCTTACGATCTGAGAGGAAATATATATATTCTTA	2034
QY	2221	CGCGTAAAGAGTGCATATAAAAATTCACAAAGCTGTCAACACACAAAGAAAGAAATCAATA	2280
Db	2035	CGCGTAAAGAGTGCATATAAAAATTCACAAAGCTGTCAACACACAAAGAAAGAAATCAATA	2094
QY	2281	AGATCAAGAAATTTATATCAATTTGCTCAATTTATGAGAACTTTCTAGAAATTTCTAGAA	2340
Db	2094	AGATCAAGAAATTTATATCAATTTGCTCAATTTATGAGAACTTTCTAGAAATTTCTAGAA	2154
QY	2341	ATAAATTCAGATGCTATGTAACAGAGAGAGTGGTGGTGTCAAAAAGAGAGTGGTGAAGAGAG	2400
Db	2155	ATAAATTCAGATGCTATGTAACAGAGAGAGTGGTGGTGTGTCAAAAAGAGAGTGGTGAAG	2214
QY	2401	CGTCTAAACACATGAAAAAATATAGTTTATATATGAGAGATCAGATGAAAGATATGAA	2460
Db	2215	CGTCTAAACACATGAAAAAATATAGTTTATATATGAGAGATCAGATGAAAGATATGAA	2274
QY	2461	AGTAAACATCTCCACAGAGAGAGTGCAGAAATTAATGATATATATGAGATACCTCAATCTA	2520
Db	2275	AGTAAACATCTCCACAGAGAGAGTGCAGAAATTAATGATATATATGAGATACCTCAATCTA	2334
QY	2521	CGAAGACGAATGCAAAAAGTGCAGAGAGAGTGCAGAGAGTGCAGAGAGTGCAGAGAGAG	2580
Db	2335	CGAAGACGAATGCAAAAAGTGCAGAGAGAGTGCAGAGAGTGCAGAGAGTGCAGAGAGAG	2394
QY	2581	AAATGAGATCTCAGAGAGCTTGGTGGACAGTGTATACAGCTTGGATTCATGATCTCTCA	2640
Db	2395	AAATGAGATCTCAGAGAGCTTGGTGGACAGTGTATACAGCTTGGATTCATGATCTCTCA	2454
QY	2641	CAGATGAGATGATTAACCTTCCACAGCTGCTGCTTCTTCAAGGACATTAATATCTTAACT	2700
Db	2455	CAGATGAGATGATTAACCTTCCACAGCTGCTGCTTCTTCAAGGACATTAATATCTTAACT	2514
QY	2701	CTTTTGTGATATAAAATGTGCATGATGAAATTTGTTTGGTGATCTGTAAGGAAATTCGA	2760
Db	2515	CTTTTGTGATATAAAATGTGCATGATGAAATTTGTTTGGTGATCTGTAAGGAAATTCGA	2574
QY	2761	ATGTTATCATCTGTTATTTATACAAATGAAAAATCTCTGTGAATCTGTGCATTTAAAA	2820
Db	2575	ATGTTATCATCTGTTATTTATACAAATGAAAAATCTCTGTGAATCTGTGCATTTAAAA	2634
QY	2821	AGTGTACAGCATTGTTCCTCTCTGCAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG	2880
Db	2635	AGTGTACAGCATTGTTCCTCTCTGCAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG	2694
QY	2881	ATGGCCCTACAGTGGAGTGGCTGATAAACAGAGCTGTCTGATATCTTGTCTCTTTTGT	2940
Db	2695	ATGGCCCTACAGTGGAGTGGCTGATAAACAGAGCTGTCTGATATCTTGTCTCTTTTGT	2754
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13 3125 TTAAATGAGGATTATTGATAT 3147
14 3141 TTTTATTTTATTTTATTTTATTTT 3183

Search completed: January 18, 2003, 04:28:58
Tab time : 129.437 secs

Genforce version 5.1.3
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10M protein nucleic search, using frame_plus.p2n model
Run on: January 18, 2003, 04:31:54 : Search time 57.7433 Seconds
(without alignments)
6107.852 Million cell updates/sec

File: us-09-026-459a-51

Perfect score: 4798

Sequence: 1 MPKPKKIAIAAAAAAEP.....TRMOKRMNDSMTSNKEEK 928

Scoring table:

Match	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Edgapop	6.0	Edgapext	7.0
Delgap	6.0	Delext	7.0

Searched: 93868 seqs, 22294149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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DB=publisedApplications_NA
-local=0
-trans-human40.cdd
-thr_min=0
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-ncpu=6
-def 11MBOUT=120
-fcgapext=7
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PublishedApplications_NA:
1: /cpnz6/prodat/a1/pubpna/mcn7_purc_mr_seq
2: /cpnz6/prodat/a1/pubpna/pet_new_purc_seq
3: /cpnz6/prodat/a1/pubpna/us06_npw_purc_seq
4: /cpnz6/prodat/a1/pubpna/us06_purc_omr_seq
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14: /cpnz6/prodat/a1/pubpna/us06_purc_omr_seq

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	4798	100.0	4554	10	US-09-469-522-50 Sequence 50, Appl
2	4787	99.8	4555	10	US-09-469-522-40 Sequence 1, Appl1
3	4787	99.8	4839	9	US-09-954-531-143 Sequence 143, App
4	4777	99.6	2995	10	US-09-860-211-7 Sequence 7, Appl1

5	4599	95.9	3455	10	US-09-469-522-28 Sequence 28, Appl1
6	4595.5	95.8	3461	10	US-09-469-522-40 Sequence 40, Appl1
7	4489	93.6	3392	10	US-09-469-522-40 Sequence 30, Appl1
8	4444.5	92.6	3477	10	US-09-469-522-46 Sequence 46, Appl1
9	4337.5	91.7	3384	10	US-09-469-522-48 Sequence 48, Appl1
10	4398.5	91.7	3347	10	US-09-469-522-42 Sequence 42, Appl1
11	4357	90.8	3323	10	US-09-469-522-42 Sequence 38, Appl1
12	4323.5	90.1	3323	10	US-09-469-522-48 Sequence 48, Appl1
13	4263	88.8	3266	10	US-09-469-522-44 Sequence 34, Appl1
14	4192	87.4	3218	10	US-09-469-522-44 Sequence 3, Appl1
15	4088.5	84.8	3161	10	US-09-469-522-44 Sequence 44, Appl1
16	4017	83.7	3113	10	US-09-469-522-46 Sequence 36, Appl1
17	810.5	16.9	3960	9	US-09-292-758-37 Sequence 37, Appl1
18	516.5	10.8	3747	12	US-09-770-657-1 Sequence 1, Appl1
19	516.5	10.8	3747	12	US-10-025-676-2 Sequence 2, Appl1
20	384.5	8.0	3259	10	US-09-220-091-4 Sequence 4, Appl1
21	243	5.1	411	10	US-09-864-761-131 Sequence 131, Ap
22	218	4.5	129	10	US-09-864-761-131 Sequence 131, Ap
23	177.5	3.7	304	10	US-09-964-824A-296 Sequence 296, App
24	156	3.3	8493	9	US-10-071-766-51 Sequence 51, Appl
25	152	3.2	10096	10	US-09-960-254-163 Sequence 163, App
26	148.5	3.1	3624	9	US-10-108-605-216 Sequence 216, App
27	147	3.1	10190	10	US-09-864-864-292 Sequence 292, App
28	147	3.1	10211	10	US-09-954-456-1153 Sequence 1153, Ap
29	147	3.1	10211	10	US-09-967-788A-186 Sequence 186, App
30	146	3.0	6773	10	US-09-864-864-336 Sequence 336, App
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33	144.5	3.0	7792	12	US-10-044-090-459 Sequence 459, App
34	144	3.0	5864	10	US-09-864-864-405 Sequence 405, App
35	141	2.9	4754	10	US-09-982-091A-1 Sequence 1, Appl1
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37	138.5	2.9	2647	10	US-09-815-242-9859 Sequence 9859, Ap
38	134.5	2.8	2526	9	US-09-948-842A-1242 Sequence 1242, Ap
39	134	2.8	6524	10	US-09-821-326-57 Sequence 55, Appl1
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41	131.5	2.7	3865	10	US-09-604-287A-474 Sequence 474, App
42	131.5	2.7	3865	12	US-10-007-805-474 Sequence 474, App
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44	131.5	2.7	4352	10	US-09-801-308-59 Sequence 59, Appl1
45	131.5	2.7	4458	12	US-10-007-805-564 Sequence 564, App

ALIGNMENTS

RESULT 1
US-09-469-522-50
Sequence 50, Application US/09/469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhong, Yunli
TITLE OF INVENTION: METHOD FOR IDENTIFYING A LOW-R COMPRESSOR PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT, WHITE & PARKER
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.00
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec 1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/0626,459
 FILING DATE: <UNKNOWN>
 ALTERNATE/APPNO INFORMATION:
 NAME: Hibert, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UTG:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3554 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURES:
 NAME/KEY: CDS
 LOCATION: 7..2790
 SEQUENCE DESCRIPTION: SEQ ID NO: 50:

US 09 459 522 50

Alignment Scores:

Prod. Name: 0 Length: 3554
 Score: 4798.00 Matches: 928
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

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 DB 67 CTGACACCG 126
 QY 41 AspleuProLeuValArgLeuGluPheGluGluThrGluGluProAspPheThrAlaLeu 60
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 QY 61 CysGlnLysLeuLysLeuThrAspHisValArgGluArgAlaThrProLeuThrProLeuLys 80
 DB 187 TGCACAAATTAACATATACATATATATATATATATATATATATATATATATAT 246
 QY 81 ValSerSerValAspGlyValLeuGlyGlyGlyTyrIleGlnLysLysLysLeuThrProGly 100
 DB 247 GTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 306
 QY 101 IleCysIlePheIleAlaValAspLeuGlyAspMetSerPheThrPheThrGluLeu 120
 DB 437 ATGTGATCTTATATGACACATGACCTAGGTGATATGCTGCTGCTGCTGCTGCTG 366
 QY 121 GlnLysAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThr 140
 DB 467 CAGAAAAACAACAAATACATGCTCCCAAAATATCTTAATCTACTAAAAACAATGATACC 426
 QY 141 SerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAla 160
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 QY 181 IleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeu 200
 DB 547 ATATCTACGAAATTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 606
 QY 201 AlaLysGlyValLeuLeuAlaMetGlnAspLeuValIleSerThrGlnLeuMetLeu 220

DB 607 GCTAAAGGAGAAATATTATAAAGGAGAGATGATGCTGATTCATTTTCAGTTAATGCTA 666
 QY 221 CysValIleAspTyrPheIleLysLeuSerPhePheMetIleLysLeuLysLeuLys 240
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 DB 727 ACAGCTGTAT 786
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 QY 321 TyrGlnGluIleLysLeuLysAspGluAspAlaArgLeuLeuLeuLeuLeuLeuLeu 340
 DB 967 TATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1026
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[illegible]

1 SOFTWARE: Patent in Release #1.0, Version #1.30
 2 CURRENT APPLICATION DATA:
 3 APPLICATION NUMBER: US 09/469,522
 4 FILING DATE: 22-Dec-1999
 5 CLASSIFICATION: <Unknown>
 6 PRIOR APPLICATION DATA:
 7 APPLICATION NUMBER: 09/026,459
 8 FILING DATE: <Unknown>
 9 ATTORNEY/AGENT INFORMATION:
 10 NAME: Hilder, David W.
 11 REGISTRATION NUMBER: 41,071
 12 REFERENCE/DOCKET NUMBER: UDC:506
 13 TELECOMMUNICATION INFORMATION:
 14 TELEPHONE: 512/418-3000
 15 TELEFAX: 512/474-7577
 16 E-MAIL FOR SEQ ID NO: 30:
 17 SEQUENCE CHARACTERISTICS:
 18 LENGTH: 3392 base pairs
 19 TYPE: nucleic acid
 20 STRANDEDNESS: single
 21 TOPOLOGY: linear
 22 FEATURE:
 23 NAME/KEY: CDS
 24 LOCATION: 7..32628
 25 SEQUENCE DESCRIPTION: SEQ ID NO: 30:
 26 US-09-469-522-30

Alignment Scores:
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 256 GlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGlnAsnAspThrAlaIleGlu 275
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 276 ValLeuGlyGlnGlnHisGlnCysAsnIleAspGlnValLysAsnValTyrPheLysAsn 295
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 296 PheIlePheProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGlu 315
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 376 ArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGln 395
 970 AGCAGCTGTATGACACATACCAACAAATTAATGATGATGATGATGATGATGATGAT 1029
 396 ProSerGluAsnLeuLeuSerTyrPheAsnAsnCysThrValAsnProLysGlnSerIle 415
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 1150 CAGGCTGTGTGTGAAATTTGATACAGGATACAAACCTGAGTGTGCTGATTAAGCCA 1209
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 1210 GTAATGGAATCATGATTATTAATCAAGAAAGAAAGATTAATCAATCAAAATTTTAC 1269
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 1270 CTCTGAAATCAAAATTTTATTAATGATGATGATGATGATGATGATGATGATGAT 1329
 496 AlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPhePro 515
 1330 GTCATATACAGAGAGATACATCAGATCTGATCTGGAACAGATTTGCTGTTCCCA 1389
 516 TrpIleLeuAsnValIleAsnLeuLysAlaPheAspPheTyrLysValIleGlnSerPhe 535
 1390 TGCATCTCAATGCTTAATTTAAAGAGCTTTGATTTTACAAAGATGATGGAAGTTT 1449
 536 IleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisIleGluArgCysGluHis 555
 1450 ATCAAGATCAAGAGAAATTTGACAAAGAAATGATTAAGAAATTTGAGCAATGATGAT 1509
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RESULT 11
US-09-469-522-32
Sequence 32, Application US/09469522
Patent No. US20040151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Xue
Ho, Shi-Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US2004/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: C01N000000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/LOCAL NUMBER: UICX:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3323 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2559
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-469-522-32
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Sequence 44, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
Applicant Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli

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GenCore version 5.1.1.3
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Gapop 10.0, Gapext 1.0

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	4443.8	96.9	3455	10	US-09-469-522-38 Sequence 28, Appl
5	4379.8	95.1	3392	10	US-09-469-522-30 Sequence 30, Appl
6	4361.6	94.3	3461	10	US-09-469-522-40 Sequence 40, Appl
7	4311.8	93.2	3424	10	US-09-469-522-42 Sequence 32, Appl
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13	4126.8	88.0	3447	10	US-09-469-522-42 Sequence 42, Appl
14	4107	87.4	3113	10	US-09-469-522-36 Sequence 36, Appl
15	2853.2	80.3	2995	10	US-09-860-211-7 Sequence 7, Appl
16	2827.4	79.6	3181	10	US-09-469-522-44 Sequence 44, Appl
17	428	12.0	451	9	US-09-756-692-7740 Sequence 7740, Ap
18	142.2	4.0	411	10	US-09-864-761-4141 Sequence 3131, Ap
19	129	3.6	129	10	US-09-864-761-19410 Sequence 19510, A

20	104	2.9	304	10	US-09-964-824A-296	Sequence 296, App
21	68.8	1.9	3960	9	US-09-292-758-37	Sequence 37, Appl
22	59.4	1.7	324	9	US-09-796-692-2546	Sequence 2546, Ap
23	51	1.4	3747	10	US-09-770-657-1	Sequence 1, Appl
24	51	1.4	3747	12	US-10-025-636-2	Sequence 2, Appl
25	49.4	1.4	640681	10	US-09-790-988-1	Sequence 1, Appl
26	48.8	1.4	345913	9	US-09-754-854A-2	Sequence 2, Appl
27	48.8	1.4	345913	9	US-09-754-854A-3	Sequence 3, Appl
28	48.4	1.4	419	10	US-09-969-373-442	Sequence 342, App
29	48.4	1.4	419	10	US-09-969-373-443	Sequence 343, App
30	48.4	1.4	513509	9	US-09-754-854A-4	Sequence 4, Appl
31	47.8	1.3	424	10	US-09-963-452-1218	Sequence 11218, A
32	47.6	1.3	411	10	US-09-960-452-14521	Sequence 14521, A
33	47	1.3	393	10	US-09-960-452-4582	Sequence 4582, Ap
34	46.2	1.3	302250	10	US-09-962-832-174	Sequence 174, Ap
35	45.8	1.3	431	10	US-09-960-452-5558	Sequence 5558, Ap
36	45.6	1.3	419	10	US-09-960-452-11244	Sequence 11244, A
37	45.4	1.3	516	10	US-09-960-452-5785	Sequence 5785, Ap
38	45.2	1.3	640681	10	US-09-790-988-1	Sequence 1, Appl
39	44.6	1.3	555	10	US-09-864-761-12458	Sequence 12458, A
40	44.6	1.3	2000	9	US-09-948-842A-2769	Sequence 2769, Ap
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42	44.4	1.2	2995	9	US-09-948-842A-4050	Sequence 4050, Ap
43	44.2	1.2	1276	10	US-09-076-927A-749	Sequence 749, App
44	44.2	1.2	2000	9	US-09-948-842A-5166	Sequence 5166, Ap
45	44.2	1.2	3209	10	US-09-220-091-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-469-522-50
: Sequence 50, Application US-094-69522
: Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli

TITLE of INVENTION: M-CELL-BLINDNESS MALE MICE WITH BLINDNESS

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4434
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-09-469-522

FILING DATE: 22-Dec-1999

CLASSIFICATION: Unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US-09-469-522

FILING DATE: Unknown

ATTORNEY/AGENT INFORMATION:

NAME: Hilber, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: 01X-506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-4000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 3554 base pairs

TYPE: nucleic acid

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1248 TATATCAAAANAGTGAAGATATAGATAATGCTTAAAGAGAAAATTTGGTAAAGTGGT 1307
1149 TATACCTCAAAAGAGTGAAGATATAGATAATGCTTAAAGAGAAAATTTGGTAAAGTGGT 1209
1308 GGCACAGGCTTCCTGCAAAATTCGATCAGACAGATACAAACCTTGGAGTTCCTGCTATTA 1367
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1428 GAACTTCGATGATGACAAACATTTTTCATGATGCTTAAATTCAGACAGAAAGATGATTC 1487
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RESULT 5

US-09-469-522-30
Sequence 40, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong Ji
Benedict, William F.
Zhou, Yuoli
TITLE OF INVENTION: MODIFIED REFINBLASTOMA HUMOR SUPPRESSOR
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09469522
FILING DATE: 22-Dec-1999
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 01X0506
TELEPHONE: 512/418-4000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 3892 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2628
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-469-522-30

Query Match 95.1% Score 3479.8; DB 10; Length 3892;
Best local Similarity 99.9%; Pred. No. 0;
Matches 3381; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 172 GATTTTATGATATGTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 241
DB 10 GATTTTATGATATGTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 69
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[illegible]

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01 4532 TTTAAATGAGATTATTAAGT 4554
02 |||||||TTTTTTTTTTTT|||
03 DB 3370 TTTAAATGAGATTATTAAGT 4492
04
05 RESULT 6
06 US-09-469-522-40
07 ; Sequence 40, Application: US-09469522
08 ; Patent No. US20020151461A1
09 ; GENERAL INFORMATION:
10 ; APPLICANT : XU, Hong Ji
11 ; Hu, Shi Xue
12 ; Benedict, William F.
13 ; Zhou, Yunli
14 ; TITLE OF INVENTION: MODIFIED PEPTINOGLYCANOMA LUMOR SUPPRESSOR
15 ; PROTEINS
16 ; NUMBER OF SEQUENCES: 51
17 ; CORRESPONDENCE ADDRESS:
18 ; ADDRESSEE: Arnold, White & Burke
19 ; STREET: P.O. Box 4434
20 ; CITY: Houston
21 ; STATE: TX
22 ; COUNTRY: USA
23 ; ZIP: 77210-4434
24 ; COMPUTER READABLE FORM:
25 ; MEDIUM TYPE: Floppy disk
26 ; COMPUTER: IBM PC compatible
27 ; OPERATING SYSTEM: PC-DOS/MS DOS
28 ; SOFTWARE: Patent In Release #1.0, Version #1.40
29 ; CURRENT APPLICATION DATA:
30 ; APPLICATION NUMBER: US-09/469,522
31 ; FILING DATE: 22-Dec-1999
32 ; CLASSIFICATION: <Unknown>
33 ; PRIOR APPLICATION DATA:
34 ; APPLICATION NUMBER: 09/026,454
35 ; FILING DATE: <Unknown>
36 ; ATTORNEY/AGENT INFORMATION:
37 ; NAME: Hibler, David W.
38 ; REGISTRATION NUMBER: 41,071
39 ; REFERENCE/DCKET NUMBER: UIC:506
40 ; TELECOMMUNICATION INFORMATION:
41 ; TELEPHONE: 512/418-3000
42 ; TELEFAX: 512/474-7577
43 ; INFORMATION FOR SEQ ID NO: 40:
44 ; SEQUENCE CHARACTERISTICS:
45 ; LENGTH: 3461 base pairs
46 ; TYPE: nucleic acid
47 ; STRANDEDNESS: single
48 ; TOPOLOGY: linear
49 ; FEATURE:
50 ; NAME/KEY: CDS
51 ; LOCATION: 7..2697
52 ; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
53 US-09-469-522-40

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QY 3301 GTCAAAAG 3360
Db 3094 GTCAAAAG 3153

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 STREET: Two Embarcadero Center, Eighth Floor
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 STATE: California
 COUNTRY: USA
 ZIP: 94111 3944

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/860,211
 FILING DATE: 18 May 2001
 CLASSIFICATION: Unknown

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/428,673
 FILING DATE: 15 Feb 2000
 APPLICATION NUMBER: US 08/142,669
 FILING DATE: 25 Oct 1993
 APPLICATION NUMBER: US 08/233,669
 FILING DATE: 26 Apr 1994

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 REFERENCE/DOCKET NUMBER: 016949 0652005

TELECOMMUNICATION INFORMATION:
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 TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 295 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURES:

NAME/KEY: CUS
 LOCATION: 149..295
 OTHER INFORMATION: /product = "RR"
 Note = "retinoblastoma tumor suppressor"

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Query Match 80.4% Score 2853.2; DB 10; Length 295;
 Best Local Similarity 99.9% Pred. No. 0;
 Matches 2853; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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us-09-026-459a-30

January 16, 2003, 15:20:22 : Search time 92.6665 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	3383	99.7	3355	10	US-09-469-522-28 Sequence 28, Appl
3	3383	99.7	3355	10	US-09-469-522-1 Sequence 1, Appl
4	3383	99.7	4839	9	US-09-954-531-143 Sequence 143, Appl
5	3379.8	99.6	3554	10	US-09-469-522-50 Sequence 50, Appl
6	3315	97.7	3323	10	US-09-469-522-32 Sequence 32, Appl
7	3257	95.9	3295	10	US-09-469-522-44 Sequence 44, Appl
8	3226	95.1	3323	10	US-09-469-522-48 Sequence 48, Appl
9	3225.4	95.1	3461	10	US-09-469-522-40 Sequence 40, Appl
10	3212	94.7	3218	10	US-09-469-522-3 Sequence 3, Appl
11	3167	91.6	3113	10	US-09-469-522-36 Sequence 36, Appl
12	3024.6	89.2	3383	10	US-09-469-522-46 Sequence 46, Appl
13	3012.6	88.8	3377	10	US-09-469-522-46 Sequence 46, Appl
14	3006	88.6	3347	10	US-09-469-522-12 Sequence 12, Appl
15	2827.4	83.4	3161	10	US-09-469-522-44 Sequence 44, Appl
16	2686.4	79.2	2995	10	US-09-860-211-7 Sequence 7, Appl
17	428	12.6	451	9	US-09-796-692-7740 Sequence 7740, Ap
18	142.2	4.2	411	10	US-09-864-761-3141 Sequence 3141, Ap
19	129	3.8	129	10	US-09-864-761-19910 Sequence 19910, A

20	104	3.1	394	10	US-09-064-824A-296 Sequence 296, App
21	68.8	2.0	3940	9	US-09-292-758-37 Sequence 37, Appl
22	59.4	1.8	324	9	US-09-796-692-2546 Sequence 2546, Ap
23	51	1.5	3747	10	US-09-770-657-1 Sequence 1, Appl1
24	51	1.5	3747	12	US-16-525-476-2 Sequence 2, Appl1
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29	48.4	1.4	419	10	US-09-969-373-443 Sequence 343, App
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33	47	1.4	393	10	US-09-960-352-4582 Sequence 4582, Ap
34	46.2	1.4	302259	10	US-09-962-832-154 Sequence 154, App
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45	44.2	1.3	3209	10	US-09-220-091-4 Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-469-522-30
Sequence 30, Application: US/95459522
Patent: NO. US20020151461A1
GENERAL INFORMATION:

APPLICANT: Xu, Hong Ji
Hu, Shi-xue
Benedict, William F.
Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4434

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4434

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/99/469-522

FILING DATE: 22-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hübner, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UIXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-4000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 3392 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2628
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-459-522-30

Query Match 100.0% Score 3392; DB 10; Length 3392;
Best Local Similarity 100.0% P-adj No. 0
Matches 3392; Conservative 0; Mismatches 0; Gaps 0;
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DB 1 GGCATCATGATTTTATGCTATATGTCAGAAATTAATAATATGATATGTCAGAGAG 60
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DB 901 ACACAGAGAACCCGAAAAATTAACCTTGATGAGAGCTGAATCTAATTTCTGCAAC 960
QY 961 ACTCCAGTTAGCAGCTGTTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 1020
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DB 1021 AGTATGCTAAAGCTTCAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080
QY 1081 GAAATATATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1140
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QY 1141 GCTTGGGATGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB 1141 GCTTGGGATGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1201 TATTACGAGTAATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1260
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QY 1261 TTTAGCAAACTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
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QY 1441 GAAATTTTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 1500
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DB 1501 TGTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
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DB 1801 AATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
QY 1861 CACCCAGAAATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
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QY 1921 GAAATTTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 1980
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QY 1981 AATCTGAGTAATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2040
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 Db 1410 AATGATAAACATTTTAAAGGATGTAAGATCAATCAATGGAATGCTTGCATGCTCTC 1469
 QY 1549 AGATTCACCTTTTATTTTATTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1598
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 QY 1599 GCTTCGAATGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1658
 Db 1540 GCTTCGAATGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1589
 QY 1659 GTATCTTCCTCTGTATGATCTGCAAGAAAGGTTTCAATGAGGTTGTAATTCATC 1718
 Db 1590 GTATCTTCCTCTGTATGATCTGCAAGAAAGGTTTCAATGAGGTTGTAATTCATC 1649
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 QY 1779 GTCT 1838
 Db 1710 GTCT 1769
 QY 1809 TGTGAAATGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1868
 Db 1770 TGTGAAATGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1829
 QY 1899 GCAATGCAAGATCAATGATCAATGATCAATGATCAATGATCAATGATCAATGATCAAT 1958
 Db 1840 GCAATGCAAGATCAATGATCAATGATCAATGATCAATGATCAATGATCAATGATCAAT 1889
 QY 1959 GTGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2018
 Db 1890 GTGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1949
 QY 2019 AACATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2078
 Db 1950 AACATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2009
 QY 2079 AGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2138
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 QY 2139 AACATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2198
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 QY 2379 GATTCACCTCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2438
 Db 2310 GATTCACCTCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2369
 QY 2439 AACATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2498
 Db 2370 AACATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2429
 QY 2499 ACATTCACCTCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2558

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 QY 2559 TTCTACTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2618
 Db 2490 TTCTACTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2549
 QY 2619 GGAACAGAAATGAGGATCTTCCAGCAGCTTGGGACACTTGGACACTTGGACACTTGGAC 2678
 Db 2550 GGAACAGAAATGAGGATCTTCCAGCAGCTTGGGACACTTGGACACTTGGACACTTGGAC 2609
 QY 2679 TCTCTCAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2738
 Db 2610 TCTCTCAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2669
 QY 2739 TCCAGTCTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2798
 Db 2670 TCCAGTCTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2729
 QY 2799 ACTTGAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2858
 Db 2730 ACTTGAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2789
 QY 2859 TTTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2918
 Db 2790 TTTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2849
 QY 2919 AGTAAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2978
 Db 2850 AGTAAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2904
 QY 2979 TCTTTGTAGCATATAGGTCATGATGATGATGATGATGATGATGATGATGATGATG 3038
 Db 2910 TCTTTGTAGCATATAGGTCATGATGATGATGATGATGATGATGATGATGATGATG 2969
 QY 3039 TTTTAAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3098
 Db 2970 TTTTAAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3029
 QY 3099 TTTTAAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3158
 Db 3030 TTTTAAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3089
 QY 3159 ATTAGAAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3218
 Db 3090 ATTAGAAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3149
 QY 3219 ACTTGTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3278
 Db 3150 ACTTGTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3209
 QY 3279 AATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3338
 Db 3210 AATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3269
 QY 3339 TACTGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3392
 Db 3270 TACTGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3323

RESULT 9

US-09-469-522-40

: Sequence 40, Application US/09449522

: Patent No. US20020151461A1

: GENERAL INFORMATION:

: APPLICANT: Xu, Hong-Ji

: Hu, Shi-Xue

: Benedict, William F.

: Zhou, Yunli

: TITLE OF INVENTION: MODIFIED EFTIN-GLASTOMA TOW-P SUPPRESSOR

: PROTEINS

: NUMBER OF SEQUENCES: 51

: CORRESPONDENCE ADDRESS:

REFERENCE/KEY NUMBER: DTIC:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418 4000
 TELEFAX: 512/474 7577
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2454
 SEQUENCE DESCRIPTION: SEQ ID NO: 43:
 US 09 469 522 4

Query Match 94.7% Score 4212; DB 10; Length 4218;
 Best Local Similarity 100.0% Pred. No. 0;
 Matches 4212; Conservation 0; Mismatches 0; Gaps 0;

181 AAGGCGGACGCTTATGAGTACAGAAAACATAGAAATACGCTGCCATAAAATCTTT 240
 182 AAGGCGGACGCTTATGAGTACAGAAAACATAGAAATACGCTGCCATAAAATCTTT 66
 241 AATTACTAAGAAATGATACAGTACGAAAGTTGATATGCTATGTCAGACTGTTG 300
 67 AATTAATTAAGAAATGATACAGTACGAAAGTTGATATGCTATGTCAGACTGTTG 126
 301 AAGAGATATGATGATGCTTATGAGTACAGAAAACATAGAAATACGCTGCCATAAAATCTTT 360
 127 AAGAGATATGATGATGCTTATGAGTACAGAAAACATAGAAATACGCTGCCATAAAATCTTT 186
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 DB 847 AGTGATCAACCTTCAGAAAAATCATTTCTTATTAATCAATCAATCAATCAATCAAT 906
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 DB 1627 AACTGAGCTTCCAGCAAGGCAATTTGATCAAGGCAAGGCAATTTGATCAAGGCA 1686
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 DB 1687 AACTGAGCTTCCAGCAAGGCAATTTGATCAAGGCAAGGCAATTTGATCAAGGCA 1746
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QY 2161 TCCAGCAGAGCCCTGAGCTGTCACCAATACCTCACAATGCTGCAAGCCCTTACAAGTTT 2220
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QY 2441 TATATAATTTTCAAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
10 2167 TATATAATTTTCAAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2226
QY 24 1 TATATAATTTTCAAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2480
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QY 2461 TATATAATTTTCAAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
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QY 2821 TATATAATTTTCAAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
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QY 2881 TATATAATTTTCAAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940
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QY 2941 TATATAATTTTCAAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000
10 2767 TATATAATTTTCAAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2826
QY 3001 TATATAATTTTCAAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3060
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QY 3061 TATATAATTTTCAAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120
10 2887 TATATAATTTTCAAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2946
QY 3121 TATATAATTTTCAAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3180
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QY 3181 TACACATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 3240
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QY 3241 TTTTGGCTTTTAAATATAAATAAAGCTGCAAGCAAGATATAACCAATATACATATATAT 3300
Db 3067 TTTTGGCTTTTAAATATAAATAAAGCTGCAAGCAAGATATAACCAATATATATATATAT 3126
QY 3301 ACTGAACACATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 3360
Db 3127 ACTGAACACATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 3186
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RESULT 11
US-09-469-522-36
Sequence 36, Application: US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SHOWNCHS: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4133
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CREATING SYSTEM: PC DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09469 522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 01XG:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474 7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3113 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2349
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-469-522-36

Query Match 91.6%; Score 3107; DB 10; Length 3113;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 AGTCACACACTGTGTGAAGAAGTATGATGTTTGTGCACTCTTCAGCAAAATTGCAAAAG 345

16 592 ATCAATTTTATTAGCTAAAGGAGATATTAAATGGAGATGATCTGGTATTCA 651
QY
17 490 TTTCAGTAAAGTATGCTGCTGACATATTTATTAACATCTCAGCTGGCTGCTC 549
DB
18 652 TTTCAGTAAAGTATGCTGCTGACATATTTATTAACATCTCAGCTGGCTGCTC 711
QY
19 550 AAATAGGATATATAAAGTATTTATATATATATATATATATATATATATATAT 609
DB
20 712 AAATAGGATATATAAAGTATTTATATATATATATATATATATATATATATAT 740
QY
21 610 GTTTCAT 669
DB
22 741 GTTTCAT 740
QY
23 670 GTTTCAT 729
DB
24 741 GTTTCAT 740
QY
25 740 TTTATAGCTTTTATGATCTCTTGGAGCTGTATCATCTATATGACTTCTAGAGTTGAA 789
DB
26 741 TTTATAGCTTTTATGATCTCTTGGAGCTGTATCATCTATATGACTTCTAGAGTTGAA 780
QY
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DB
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30 841 TTTTGGAT 900
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APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTXC:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-4000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 3347 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 7..2583
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-469-522-42
Query Match 84.6%; Score 3026; DB 10; Length 3347;
Best Local Similarity 100.0%; Pred No 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 342 ATCTACTGAAATAAAATTTGTTTGGTAAAGTTTGGTAAAGTTTGGTAAAGTTTGGTAAAG 401
QY 447 TAAAGGGAAGTATTAATAAGGAGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 506
DB 402 TAAAGGGAAGTATTAATAAGGAGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 461
QY 507 TGTCTTGGTATTTATTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 566
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RESU.1 14
US 09 469 522-42
Sequence 42 App. 09/026/459a-30/2994/9522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong Ji
Ho, Shi-xue
Hendrick, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENT ADDRESS:
ADDRESSEE: Arnold, White & Barker
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In. P-1-usp #1 0 V-1-usp #1 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: mpf:mw
PRIOR APPLICATION DATA:



QY 702 ValGlnGlnThrPheGlySerValLeuAlaGlyGluGluThrAspSerIleIleVal 721
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 QY 742 PheTyrAsnSerValPheMetGlnArgGluIleYThrAsnIleLeuGlnTyrAlaSerThr 741
 Db 2401 TGTATAAATCGGCTCTTCATGACACATATCAAAACAAATATTTGACAGTATGCTCCACC 2450
 QY 742 ArgProThrLeuSerPheIleProHisIleProArgSerProTyrIleYThrPheProSer 761
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 Db 2581 ALTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
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RESULTS 5

US-09-469-522-50
 1 Sequence 50 Application US-09-469-522
 2 Patent No. US2626151461A1
 3 GENERAL INFORMATION:
 4 APPLICANT: Xu, Hong Ji
 5 Hu, Shi-Xue
 6 Hensdict, William P
 7 Zhou, Yunli
 8 TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

NUMBER OF SEQUENCES: 51
PROTEINS

1 CORRESPONDENCE ADDRESS:
 2 ADDRESSEE: Arnold, White & Durkee
 3 STREET: P.O. Box 4433
 4 CITY: Houston
 5 STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1 0, Version #1 30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-09-469-522

FILING DATE: 22-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026-459

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

1 NAME: Hibler, David W.
 2 REGISTRATION NUMBER: 41,071
 3 REFERENCE/DOCKET NUMBER: UIXU-506
 4 TELECOMMUNICATION INFORMATION:
 5 TELEPHONE: 512/418-3000
 6 TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 3554 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CUS

LOCATION: 7..2790

SEQUENCE DESCRIPTION: SEQ ID NO: 50:

US-09-469-522-50

Alignment Scores:

Pred. No.: 0

Score: 4599.00

Percent Similarity: 99.63%

Best Local Similarity: 99.78%

Query Match: 99.67%

Indels: 0

Gaps: 10

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Matches: 892

Conservative: 1

Mismatches: 1

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Gaps: 0

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QY 62 LysLysGlnLeuTrpGlyIleCysIlePheIleAlaAlaValAspLeuAspLeuMetSer 81

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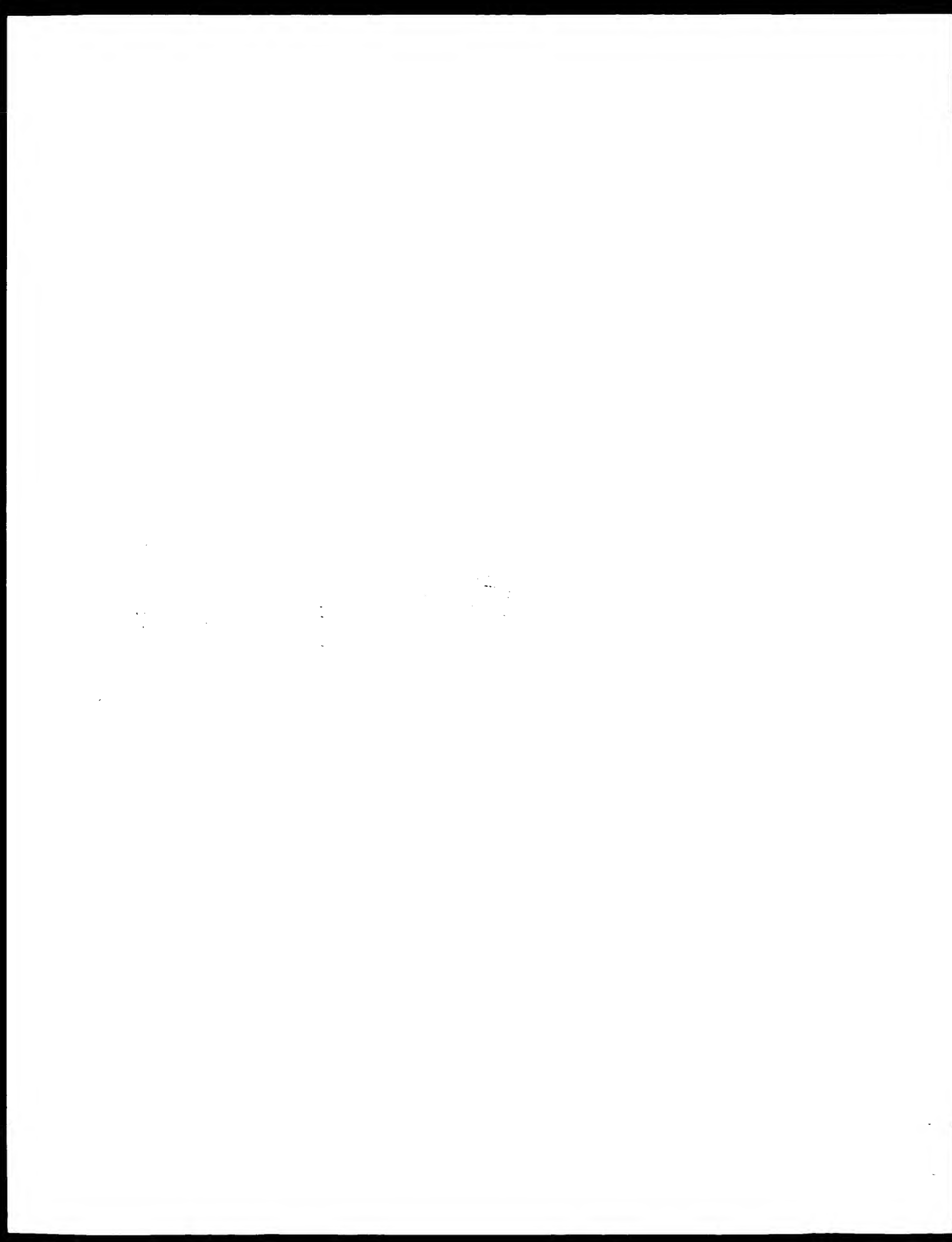
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1607 AAG 2454

RESULT 16
US 09-026-459a-29
Sequence 36, Application US/09469522
Patent No. US2003015146A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F
Zhou, Yunli
TITLE & INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09469522
FILING DATE: 22-Dec-1999
CLASSIFICATION: (Unknown)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: (Unknown)
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
FIRM/INSTITUTION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 01X:506
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3113 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2349
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-469-522-36
Alignment Scores:
Pred. NO.: 0 Length: 4113
Score: 4017.00 Matches: 781
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.06% Indels: 0
DB: 10 Gaps: 0
US-09-026-459a-29 (1-895) x US 09-469-522-36 (1-4113)

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Db 67 ACATGTCAACAT 126
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Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NAs*

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SUMMARIES

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3	4447	99.8	4849	9	US-09-954-531-143 Sequence 14, Appl
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5	4443	97.9	3492	10	US-09-469-522-42 Sequence 36, Appl
6	4415	95.9	4324	10	US-09-469-522-42 Sequence 32, Appl
7	4297	94.3	4266	10	US-09-469-522-40 Sequence 34, Appl
8	4247.8	94.0	4461	10	US-09-469-522-40 Sequence 40, Appl
9	4226	93.4	4324	10	US-09-469-522-48 Sequence 38, Appl
10	4212	93.0	4218	10	US-09-469-522-48 Sequence 37, Appl
11	4107	89.9	3113	10	US-09-469-522-46 Sequence 36, Appl
12	4088.6	89.4	3484	10	US-09-469-522-48 Sequence 48, Appl
13	4076.6	89.0	3477	10	US-09-469-522-46 Sequence 46, Appl
14	4019.8	87.4	3347	10	US-09-469-522-42 Sequence 42, Appl
15	2827.4	81.8	3161	10	US-09-469-522-44 Sequence 44, Appl
16	2759.4	79.6	2995	10	US-09-860-211-7 Sequence 7, Appl
17	4268	12.4	451	9	US-09-736-692-7740 Sequence 7740, Ap
18	142.2	4.1	411	10	US-09-864-761-3131 Sequence 3131, Ap
19	129	3.7	129	10	US-09-864-761-1910 Sequence 1910, A

Sequence 296, App
Sequence 37, Appl
Sequence 2546, Ap
Sequence 1, Appl
Sequence 2, Appl
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Sequence 3, Appl
Sequence 342, App
Sequence 343, App
Sequence 4, Appl
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Sequence 4582, Ap
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Sequence 4050, Ap
Sequence 749, App
Sequence 5166, Ap
Sequence 4, Appl

104 3.0 304 10 US-09-964-824A-296
21 68.8 2.0 3960 9 US-09-292-758-37
22 59.4 1.7 324 9 US-09-794-592-2546
23 51 1.5 3747 10 US-09-770-657-1
24 51 1.5 3747 12 US-10-025-676-2
25 49.4 1.4 640681 10 US-09-790-988-1
26 48.8 1.4 345913 9 US-09-754-854A-2
27 48.8 1.4 345913 9 US-09-754-854A-2
28 48.4 1.4 419 10 US-09-969-373-442
29 48.4 1.4 419 10 US-09-969-373-442
30 48.4 1.4 513509 9 US-09-754-854A-4
31 47.8 1.4 424 10 US-09-960-352-11218
32 47.6 1.4 411 10 US-09-960-352-11218
33 47 1.4 393 10 US-09-960-352-11218
34 46.2 1.3 352250 10 US-09-962-842-154
35 45.8 1.3 431 10 US-09-960-352-11218
36 45.6 1.3 419 10 US-09-960-352-11218
37 45.4 1.3 516 10 US-09-960-352-11218
38 45.2 1.3 640681 10 US-09-790-988-1
39 44.6 1.3 555 10 US-09-864-761-17658
40 44.6 1.3 2000 9 US-09-948-842A-2769
41 44.6 1.3 2000 9 US-09-948-842A-4147
42 44.4 1.3 2000 9 US-09-948-842A-4050
43 44.2 1.3 1376 10 US-09-070-927A-749
44 44.2 1.3 2000 9 US-09-948-842A-5166
45 44.2 1.3 3209 10 US-09-220-091-4

ALIGNMENTS

RESULT 1

US-09-469-522-28

Sequence 28, Application 28/09469522

Patent No. US-09-0151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong Ji

Hu, Sha-Xue

Honedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MAMMARY KILINOMATOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Burke

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent to Release #1.0, Version #1.40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09469522

FILING DATE: 22 Dec 1999

CLASSIFICATION: Unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: Unknown

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: 01X0596

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/474-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 3455 base pairs

TYPE: nucleic acid

US 09-469,522-1
SEQUENCE DESCRIPTION: SEQ ID NO: 1;

Query Match: 99.8%; Score 3447; DB 10; Length 3555;
Best local similarity 100.0%; Pred. NC. 0;
Matches 3447: Conservative 0; Mismatches 0; Indels 0;

0:

[illegible]

D6	1068	GAGAACACCAGAAAAAGTAACCTTGATGAGAGAGGTGAAAGCTAAATGCTGCTCCACACACG	1122
QY	1029	AGTTAGAGACTGTTATGAGCACTAAGCAACTAATATGATGATTTTAAATTCAGCAAAATGGA	1089
DB	1128	AATTAGCAATGTTATGAAACATATGACACAAATATGATGATTTTAAATTTAGCAATGGA	1187
QY	1089	TCACCTTTCAGAAAAATCTGATTTGCTTATTTTAACTGCACAGTGAATGCAAAAAGAG	1148
DB	1188	TATACTCAAAAGAGTGAAGCATATAGATACATCTTTAAACAGAAATTTGTAAGATGTG	1247
QY	1269	CCGAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1328
DB	1248	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1307
QY	1209	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1268
DB	1308	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1367
QY	1269	CCGAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1328
DB	1368	CCGAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1427
QY	1329	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1388
DB	1428	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1487
QY	1389	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1448
DB	1488	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1547
QY	1449	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1508
DB	1548	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1607
QY	1509	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1568
DB	1608	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1667
QY	1569	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1628
DB	1668	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1727
QY	1629	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1688
DB	1728	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1787
QY	1689	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1748
DB	1788	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1847
QY	1749	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1808
DB	1848	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1907
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DB	1908	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1967
QY	1869	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1928
DB	1968	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	2027
QY	1929	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	1988
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QY	1989	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	2048
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QY	2049	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	2108
DB	2148	GAAGTGAATGGAATTCATGATATAGATACATCTTTAACTGCACAGTGAATGCAAAAAGAG	2207

[illegible]

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1  RESULT 7
2  US 09/469,522 44
3  Sequence 44, Application US/09469522
4  Patent No. US2002015491A1
5  GENERAL INFORMATION:
6  APPLICANT: Xu, Hong Ji
7  Ho, Shi Xue
8  Benedict, William F.
9  Zhou, Yanli
10 TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR
11
12 NUMBER OF SEQUENCES: 51
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: Arnold White & Dwyer
15 STREET: P.O. Box 4434
16 CITY: Houston
17 STATE: TX
18 COUNTRY: USA
19 ZIP: 77210-4434
20
21 COMPUTER READABLE FORM:
22 MEDIUM TYPE: Floppy disk
23 COMPUTER: IBM PC compatible
24 OPERATING SYSTEM: PC DOS/MS-DOS
25 SOFTWARE: Patent In Release #1.0, Version #1.30
26
27 CURRENT APPLICATION DATA:
28 APPLICATION NUMBER: US/09/469,522
29 FILING DATE: 22-Dec-1999
30 CLASSIFICATION: - Unknown-
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: 09/026,459
33 FILING DATE: - Unknown-
34 ATTORNEY/AGENT INFORMATION:

```


[illegible]

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 Db 678 ATATCTACGAAATATATCTGCAATGCTGCTAAAAGTTTCCTGGATCAATTTTATTA 737
 QY AlaLysGlyValLeuGlnMetGluAspLeuValIleSerPheGlnLeuMetLeu 220
 Db 738 CCAAAAGGGAACATATACAAATGGAAGATGATCTGGTCAATTCATTCAGTTAAAGCTTA 797
 QY CysValLeuAspTyrPheIleLeuLysLeuSerProMetLeuLeuLysGluProTyrLys 240
 Db 798 TGTGCTGCTGACATATTAATTAACCTGACCTCCCATGTTGCTCAAGAACATATAAA 857
 QY ThrAlaValIleProIleAsnGlySerProArgIleProArgArgGlyGlnAsnArgSer 260
 Db 858 ACAGCTGTTATAAATTAATAGTTTAATCTGAAACAAATAGAGAGATGAAACAGAGT 917
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 Db 1038 AATTCCTATGACTTTGTAATATATTAAGAGATTCAGAGAGTTCAAAATGCTTTCAAAAGA 1097
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 Db 1098 TACCAAGAAATTTATATCTAAATAATAAGATAGATGCAAGATTTATTTTGGATCATGAT 1157
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 Db 1158 AANAATCTTTCAT 1217
 QY AsnLeuAspGluGluValAsnValIleProProIleThrProValArgThrValMetAsn 380
 Db 1218 AACCTTAT 1277
 QY ThrIleGlnGlnLeuMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 400
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 Db 1338 ATTTCCTATTTTACAAATGAT 1397
 QY AspIleGlyTyrIlePheLysGlyCysPheAlaLysAlaValIleGlyCysValGlu 440
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 Db 1518 CTATAATCAAGAAAGAAAT 1577
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 Db 1638 ACTAT 1697
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 Db 1758 AACTTGACAGAGAAATGATAAAACATTTAGAACGATGTCACATCCCAATCATGAAATCC 1817
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 Db 1938 ACTGCACGAT 1997
 QY ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLys 640
 Db 1998 CCGTAAATTTCTACTCCAAATGCAGACACAAATCAACCTACAGCTTCATAGACACAAAG 2057
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 Db 2058 CATTGAATTTAT 2117
 QY ArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIle 680
 Db 2118 CGGCTAAATFACATTTCTGCAATCTCTCTGAGACACACACACACATAGACATATCATC 2177
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 Db 2538 CGAGGGAACATCAT 2597
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 Db 2598 ATCAATCAAAAT 2657
 QY ThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLys 860
 Db 2658 ACTTCTCAGAAATTCAGAGAAAATATAATCATATGATATATATATATATATATATATATATAT 2717
 QY ArgSerAlaGluLysSerAsnProProLysProLeuLysLysLeuArgPheAspIleGlu 880
 Db 2718 AGAAGTCTGAGAGGAGAGCAACCTCTCTTAAACACATCAAAAACTACGCTTTGATATCAAT 2777
 QY GlySerAspGlnAlaAspLysSerHisLeuProGlyGluGluSerPheIleGlnLys 900
 Db 2778 GATCAGATGAAAT 2837


```

1  APPLICATION NUMBER: 09/026,459
2  FILING DATE: UNKNOWN
3  ATTORNEY/AGENT INFORMATION:
4  NAME: Hibler, David W.
5  REGISTRATION NUMBER: 41,071
6  REFERENCE/DOC# NUMBER: 0180,506
7  INFORMATION INFORMATION:
8  TELEPHONE: 512/418-4000
9  TELEFAX: 512/474-7577
10 INFORMATION FOR SEQ ID NO: 50:
11     SEQUENCE CHARACTERISTICS:
12         LENGTH: 3554 base pairs
13         TYPE: nucleic acid
14         STRANDEDNESS: Single
15         TOPOLOGY: Linear
16     FEATURE:
17         NAME/KEY: CDS
18         LOCATION: 7..2790
19         SEQUENCE DESCRIPTION: SEQ ID NO: 50:
20     000 000 000 000 000 000 000 000 000 000 000 000 000 000 000 000

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581 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnAspSerHis 600
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601 ThrAlaAlaAspMetTyrLeuSerSerValArgSerProLysLysLysThrThr 620
1807 ACCTGAGCAATATCTATCTTCTGCTAAGATCTCCAAACAAACAAAGGTTCAACTACG 1866
621 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLys 640
1957 GAGGTAATAATCTACGCAAAATGACACACAAACCAACCAACCAACCAACCAACCAACCA 1926
641 ProLeuLysSerThrSerLeuSerLeuPheCysTyrLysValTyrArgLeuAlaTyrLeu 660
1957 GAGGTAATAATCTACGCAAAATGACACACAAACCAACCAACCAACCAACCAACCAACCA 1926
661 ArgLeuAsnThrLeuCysGlnAlaArgLeuSerGlnHisSerProLeuGlnHisLeuPhe 680
1957 GAGGTAATAATCTACGCAAAATGACACACAAACCAACCAACCAACCAACCAACCAACCA 1926
681 TrpThrLeuPheGlnHisThrLeuAsnAluTyrGlnLeuMetArgAspArgHisLeu 700
2047 GAGGTAATAATCTACGCAAAATGACACACAAACCAACCAACCAACCAACCAACCAACCA 2016
701 AspGlnLeuMetMetCysSerMetTyrGlyLysCysValLysValLysAsnLeuAspLeuLys 720
2107 GAGGTAATAATCTACGCAAAATGACACACAAACCAACCAACCAACCAACCAACCAACCA 2166
721 PheLysLeuLeuValPheAlaTyrLysAspLeuAlaValLeuLeuPheLys 740
2107 GAGGTAATAATCTACGCAAAATGACACACAAACCAACCAACCAACCAACCAACCAACCA 2166
741 ArgValLeuLeuLysGlnGluGluTyrAspSerLeuValPheTyrAsnSerValPhe 760
2227 GAGGTAATAATCTACGCAAAATGACACACAAACCAACCAACCAACCAACCAACCAACCA 2286
761 MetGlnAlaLeuLysThrAsnLeuLeuGlnTyrAlaSerThrArgProThrLeuSer 780
2227 GAGGTAATAATCTACGCAAAATGACACACAAACCAACCAACCAACCAACCAACCAACCA 2286
781 ArgValLeuLeuLysGlnGluGluTyrAspSerLeuValPheTyrAsnSerValPhe 800
2227 GAGGTAATAATCTACGCAAAATGACACACAAACCAACCAACCAACCAACCAACCAACCA 2286
801 GlyLysAlaLeuTyrHisSerProLeuLysSerProTyrLysLeuSerGlnLysLeuPro 820
2407 GAGGTAATAATCTACGCAAAATGACACACAAACCAACCAACCAACCAACCAACCAACCA 2466
821 ThrProThrLysMetThrProArgSerArgTyrLeuValSerIleGlyGluSerPheCly 840
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881 GlySerAspGlnAlaAspLysSerLysHisLeuProGlyGluSerLysPheGlnGlnLys 900
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901 LeuAlaLeuMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 920
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RESULT 5
US-09-469-522-28
Sequence 28, Affiliation: us/09469522
Patent NO. US29920151461A1
GENERAL INFORMATION:
Applicant: Xu, Hong-Ji
Hu, Shi-Xue
Rebedict, William E.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US, 09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09, 046,459
FILING DATE: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DRAWING NUMBER: UIC:506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 3455 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2691
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-469-522-28
Alignment Scores:
Pred. No.: 0 Length: 3455
Score: 4609.00 Matches: 894
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.08% Indels: 0
DB: 10 Gaps: 0
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QY 35 GlnAspSerGlyProGluAspLeuProLeuValArgLeuGluPheGlnGlnThrGlnGlu 54
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QY 55 ProAspPheThrAlaLeuGlySerGlnLysLeuLysIleProAspHisValArgGlnArgAla 74
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QY 75 TrpLeuThrTrpGlnLysValSerSerValAspLysValLeuGlyGlyTyrIleGlnLys 94
Db 130 TGGTAAATTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 189
QY 95 LysLysGlnLeuLeuTrpGlyIleGlySerIleGlyPheIleAlaValAspLeuAspGlnMetSer 114

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47 111 CysThrPhePheLeuAlaValAspLeuAspGluMetSerPheThrPheThrGluLeu 120
 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

461 161 LeuLysSerGluThrGluThrGluLeuSer116311641651661671681691701711721731741751761771781791801811821831841851861871881891901911921931941951961971981992002012022032042052062072082092102112122132142152162172182192202212222232242252262272282292302312322332342352362372382392402412422432442452462472482492502512522532542552562572582592602612622632642652662672682692702712722732742752762772782792802812822832842852862872882892902912922932942952962972982993003013023033043053063073083093103113123133143153163173183193203213223233243253263273283293303313323333343353363373383393403413423433443453463473483493503513523533543553563573583593603613623633643653663673683693703713723733743753763773783793803813823833843853863873883893903913923933943953963973983994004014024034044054064074084094104114124134144154164174184194204214224234244254264274284294304314324334344354364374384394404414424434444454464474484494504514524534544554564574584594604614624634644654664674684694704714724734744754764774784794804814824834844854864874884894904914924934944954964974984995005015025035045055065075085095105115125135145155165175185195205215225235245255265275285295305315325335345355365375385395405415425435445455465475485495505515525535545555565575585595605615625635645655665675685695705715725735745755765775785795805815825835845855865875885895905915925935945955965975985996006016026036046056066076086096106116126136146156166176186196206216226236246256266276286296306316326336346356366376386396406416426436446456466476486496506516526536546556566576586596606616626636646656666676686696706716726736746756766776786796806816826836846856866876886896906916926936946956966976986997007017027037047057067077087097107117127137147157167177187197207217227237247257267277287297307317327337347357367377387397407417427437447457467477487497507517527537547557567577587597607617627637647657667677687697707717727737747757767777787797807817827837847857867877887897907917927937947957967977987998008018028038048058068078088098108118128138148158168178188198208218228238248258268278288298308318328338348358368378388398408418428438448458468478488498508518528538548558568578588598608618628638648658668678688698708718728738748758768778788798808818828838848858868878888898908918928938948958968978988999009019029039049059069079089099109119129139149159169179189199209219229239249259269279289299309319329339349359369379389399409419429439449459469479489499509519529539549559569579589599609619629639649659669679689699709719729739749759769779789799809819829839849859869879889899909919929939949959969979989991000


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QY 421 TyrThrLeuGlnThrLeuLysAspLysAspLeuAstrAlaArqLeuPheLeuAspHisAsp 340
DB 1876 TGGACCCCTTTTCAGACACCTCCAGAAAGAGATGCACTCATGAGAGACAGGCAATTC 1945
QY 441 LysThrLeuGlnThrAspSerLeuAspSerPheGluThrGlnArgThrProArqLysSer 360
DB 856 AAAATTTTTCATCAATTCATTTATAGAAATAGTTTTCAGAAATAGAGAAATAGT 915
QY 461 AsnLeuAspGlnGlnValAsnValIleProProHisThrProValArgThrValMetAsn 380
DB 916 AAATTTTGAAGAGAGTGAATGTAATTCCTCCACACACTCCATAGAGAGCTTTATGAC 975
QY 481 ThrIleGlnGlnMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsnLeu 400
DB 476 ACTAATCAACAAATTAATGATCAATTAATCCACCAAGATCAACCTTCACAAAATCTG 1035
QY 491 IleSerThrPheAsnAsnCysThrValAsnProLysGlnSerIleLeuLysArqValLys 420
DB 1336 ATTTCATATTTTAACTGTAATGTAATTCCTCCACACACTCCATAGAGAGCTTTATGAC 1095
QY 491 AspIleThrThrPhePheLysGlnThrPheAlaLysAlaValGlyGlnGlyCysValGly 440
DB 1396 GATAAGATATCTTTTAAAGAAATTTTGTAAAGCTGTGGGACAGGTTGTGTGAA 1155
QY 491 ThrIleSerGlnArgThrLysLeuGlyValAlaLeuLeuTyrArgValMetGlnSerMet 460
DB 1356 ATGGATACACAGGATACAACTGGAGTTCGGCTGTGTTATACAGAGATATGCAATCCATG 1215
QY 491 LeuLysSerGlnGlnGlnArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsn 480
DB 1216 GTTAAATCAGAAATAGAAAGATATTCATCAATCAAAAATTTAGTAAATTTGTGATGACAA 1275
QY 491 ThrPheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrThrSerArg 500
DB 1276 ATTTTATAATCTTTTATTAGATGCTGCTTGTGAGTTGTAAAGCCCATATACAGAA 1335
QY 491 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnVal 520
DB 1336 AGTATGTCAGAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1395
QY 501 LeuAsnLeuLysAlaPheAspPheThrLysValIleLeuSerPheLeuValAlaGlyGly 540
DB 1396 GTTAAATTTAAAGCTTTGATTTTAAATATATATATATATATATATATATATATATATAT 1455
QY 501 AsnLeuThrArgGlnMetIleLysHisGlnArgCysGlnHisArgIleMetGlnSer 560
DB 1456 AACTTGAATACAGAAATCATAAATATTTTAAATGATGTAATATGCAATCATGCAATGCT 1515
QY 501 LeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGlu 580
DB 1516 CTTCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1575
QY 501 GlyProThrAspHisLeuGlnSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHis 600
DB 1576 GAAATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1635
QY 501 ThrAlaAlaAspMetThrLeuSerProValArgSerProLysLysLysLysSerThrThr 620
DB 1636 AATGATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1695
QY 501 ArgValAsnSerThrAlaAsnAlaGlnThrGlnAlaThrSerAlaPheGlnThrGlnLys 640
DB 1696 GGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1755
QY 501 ProLeuLysSerThrSerLeuSerLeuPheThrLysLysValTyrArgLeuAlaTyrLeu 660
DB 1756 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1815
QY 501 ArgLeuAsnThrLeuLysGlnArgLeuLeuSerGlnHisProGlnLeuGlnHisIleIle 680
DB 1816 GAAATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1875

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QY 681 TrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGlnLeuMetArgAspArgHisLeu 700
DB 1876 TGGACCCCTTTTCAGACACCTCCAGAAAGAGATGCACTCATGAGAGACAGGCAATTC 1945
QY 701 AspGlnIleMetMetCysSerMetIleCysLysValLysAsnIleAspLeuLys 720
DB 1946 GACCAAAATTTATGATGTTTCCATGATATATATATATATATATATATATATATATAT 1995
QY 721 PheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGlnThrPheLys 740
DB 1996 TTCAAAATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2055
QY 741 ArgValLeuIleLysGlnGluGluTyrAspSerIleIleValPheTyrCysSerValPhe 760
DB 2056 CGTGTGTTGATCAAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATG 2115
QY 761 MetGlnArgLeuLysThrAsnIleLeuGlnThrAlaSerThrArgProThrLeuSer 780
DB 2116 ATGCAGAGACTGAAATATAATATATTTTCAATGATGATGATGATGATGATGATGATGAT 2175
QY 781 PheIleThrPheHisThrPheAlaSerPheLysPheLeuSerSerProLeuArgIlePro 800
DB 2176 GCAATACCTCATATCTCCAGAGCCCTTACAGCTTTCCTAGTTCACCTTATGCAATTCCT 2235
QY 801 GlyGlyAsnIleThrLysSerPheLeuLysSerProTyrLysIleSerGlnIleLys 820
DB 2236 GCAAGGCAACATCATATATGACCCCTCAACACACACACATATAAAATTCACAAACCTT 2295
QY 821 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGlnSerPheGly 840
DB 2296 ACATCAATATAAATATGATTCATGATGATGATGATGATGATGATGATGATGATGATG 2355
QY 841 ThrSerGlnLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLys 860
DB 2356 ACTTCTCACAACTTCCACAAATATAACATGATGATGATGATGATGATGATGATGATGAT 2415
QY 861 ArgSerAlaGlnGlySerAsnProProLysProLeuLysLysLeuArgPheAspIleHis 880
DB 2416 ACAAAGTCTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2475
QY 881 GlySerAspGlnAlaAspGlySerThrLysHisLeuProGlyGlnSerLysPheGlnLys 900
DB 2476 GATCATATATAATATATATATATATATATATATATATATATATATATATATATATAT 2535
QY 901 LeuAlaGlnMetThrSerThrArgThrArgMetGlnLysGlnLysMetAspSerMet 920
DB 2536 CTGACACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2595
QY 921 AspThrSerAsnLysGlnGlnLys 928
DB 2596 GATACCTCAAAACAGGAAGAGAGAA 2619
RESULT 10
US-09-460-522-42
: Sequence 42, Application US/09469522
: Parent No. US2962015461A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-Ji
: Hu, Shi-xue
: Benedict, William F.
: Zhou, Yunli
: TITLE OF INVENTION: MODIFIED REFIN-GLIANTOMA TUMOR SUPPRESSOR
: PROTEINS
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

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136 736 TACGAGAAATTTATCTTAAAAATAAGATCTAGATGCAATATTATTTGGATCATGAT 795
137 741 TysThrLeuThrAspSerThrAspSerPheGluThrGlnArgThrProArgLysSer 360
138 796 AAAATCTTTCAGACTGATTTATATATATATATATATATATATATATATATATAT 855
139 861 AsnLeuAspGluValAsnValIleProProIleThrProValAlaGlnThrValMetAsn 380
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141 881 ThrIleGlnIleLeuMetIleLeuAsnSerAlaSerAspGluProSerGluAsnLeu 400
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151 481 IlePheIleMetSerIleLeuAlaCysAlaLeuValValMetAlaThrTyrSerArg 500
152 1216 AATTTCAATGATTTTAAAGCAAAATCTGTAAGCTGTCGACACAGGGTGTGTCGAA 1275
153 501 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTyrIleLeuAsnVal 520
154 1276 AGATATCTCAGAAATCTGATTTTAAAGCAAAATCTGTAAGCTGTCGACACAGGGTGTG 1335
155 521 LeuAsnLeuLysAlaPheAspPheLysValIleGlnSerPheIleLysAlaGlnGly 540
156 1336 CTAAATTTAAAGCTTTGATTTTAAAGCAAAATCTGTAAGCTGTCGACACAGGGTGTG 1395
157 541 AsnLeuThrArgGluMetIleLysIleLeuLysLysGlnLysAlaGlnMetGluSer 560
158 1396 AATTTCAAGAGATTAATGATGATTTTAAAGCAAAATCTGTAAGCTGTCGACACAGGG 1455
159 561 LeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGlu 580
160 1456 CTGATATGATTTTAAAGCAAAATCTGATTTTAAAGCAAAATCTGTAAGCTTCAAGAG 1515
161 GlyProThrAspHisLeuGlnSerAlaCysProLeuAsnLeuProGlnAsnAsnHis 600
162 1516 GAAATCAAGAGATTAATGATGATTTTAAAGCAAAATCTGTAAGCTTCAAGAGATTAAT 1575
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164 1576 AATTTCAAGAGATTAATGATGATTTTAAAGCAAAATCTGTAAGCTTCAAGAGATTAAT 1635
165 621 ArgValAsnSerThrAlaAsnAlaGlnThrGlnAlaThrSerAlaPhePheThrGlnLys 640
166 1636 GATTTCAAGAGATTAATGATGATTTTAAAGCAAAATCTGTAAGCTTCAAGAGATTAAT 1695
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168 1696 GATTTCAAGAGATTAATGATGATTTTAAAGCAAAATCTGTAAGCTTCAAGAGATTAAT 1755
169 661 ArgLeuAsnThrLeuLysGlnArgLeuLeuSerGlnLysProGlnLeuGlnLysIleIle 680
170 1756 GAGTAAATTAATGATGATTTTAAAGCAAAATCTGTAAGCTTCAAGAGATTAATGATC 1815
171 681 TrpThrLeuPheGlnLysThrLeuGlnAsnGluTyrGluLeuMetArgAspArgLysLeu 700

1816 TGGATCTTTTTCAGAC 1875
1817 701 AspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLys 720
1818 1876 GACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1935
1819 721 PheLysIleIleValThrAlaLysLysAspLeuPheIleAlaValGlnIleThrPheLys 740
1820 1936 TTTCAAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1995
1821 741 ArgValLeuIleLysGlnGluGluLysAspSerIleIleValPheLysAsnSerValPhe 760
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1823 761 MetGlnArgLeuLysIleAsnIleLeuGlnThrAlaSerThrArgProThrLeuSer 780
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1825 781 ProIleProIleIleProArgSerProTyrLysPheProSerProLeuArgIlePro 800
1826 2116 CCAATACCTTCACATGCTGCAAGAGAGAGATGATGATGATGATGATGATGATGATG 2175
1827 801 GlyGlyAsnIleTyrIleSerProLysSerProTyrLysIleSerGlnGlnLysGln 820
1828 2176 GAG 2235
1829 821 ThrProThrLysMetProArgSerArgIleLeuValSerIleGlyLysSerPheCly 840
1830 2236 ACACCAAC 2295
1831 841 ThrSerGlnLysPheGlnLysIleAsnGlnMetValTyrAsnSerArgValIleLys 860
1832 2296 ACTGTCGCAAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2355
1833 861 ArgSerAlaGlnLysSerAspProLysProLysLysLysLysLysLysLysLys 880
1834 2356 AATATGTCGAG 2415
1835 881 GlySerAspGlnAlaAspGlySerLysIleGlnThrGlnLysLysLysLysLysLys 900
1836 2416 GATTCAGATGAG 2475
1837 901 LeuAlaGlnMetThrSerThrArgMetGlnLysGlnLysMetAsnAspSerMet 920
1838 2476 CTGGAG 2535
1839 921 AspThrSerAsnLysGlnLys 928
1840 2536 GATATCTCAAAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2595

RESULT 13
US-09-469-522-34
Sequence 34, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOBLASTOMA 100P SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: HOUSTON

STATE: TX

COUNTRY: USA

ZIP: 77210 4433

COMPUTER PEAKABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1 0, Version #1. 00

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/469,522

FILING DATE: 22 Dec 1999

CLASSIFICATION: unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: unknown

ATTORNEY/AGENT INFORMATION:

NAME: Hubert, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DECKET NUMBER: 01XC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418 3000

TELEFAX: 512/474 7577

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 3161 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

Topology: linear

FEATURES:

NAME/KEY: CDS

LOCATION: 7...2497

SEQUENCE DESCRIPTION: SEQ ID NO: 44:

US 09 026 459A 2 (1 928) X US 09 469 522 44 (1-3161)

Alignment Scores:

Prod. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US 09 026 459A 2 (1 928) X US 09 469 522 44 (1-3161)

Prod. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US 09 026 459A 2 (1 928) X US 09 469 522 44 (1-3161)

Prod. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US 09 026 459A 2 (1 928) X US 09 469 522 44 (1-3161)

Prod. No.:

Score:

Percent Similarity:

Best Local Similarity:

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DB:

US 09 026 459A 2 (1 928) X US 09 469 522 44 (1-3161)

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Score:

Percent Similarity:

Best Local Similarity:

Query Match:

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US 09 026 459A 2 (1 928) X US 09 469 522 44 (1-3161)

Prod. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US 09 026 459A 2 (1 928) X US 09 469 522 44 (1-3161)

Prod. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

DB 307 AATCTATCTTTATTCACACTTCACCTA 336
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DB 336 336
QY 141 SerThrLysValAspAsnAlaMetSerAlaGluGluLysLysTyrAspValLeuPheAla 160
DB 336 336
QY 161 LeuPheSerLysLeuGluAlaThrGlyGluLeuIleTyrLeuThrGluProSerSerSer 180
DB 336 336
QY 181 HisSerThrGluIleAsnSerAlaLeuValLeuLysValSerThrPheThrPheLeuLeu 200
DB 336 336
QY 201 AlaLysGlyGluValLeuLeuHisMetGluAspPheValLeuThrPheAlaMetLeu 220
DB 336 336
QY 221 CysValLeuAspPyrPheIleLysLeuSerPheProMetLeuLeuLysGluIleThrLys 240
DB 336 336
QY 241 ThrAlaValIleProIleAsnGlySerProAlaThrProAlaAspGlyGluAsnAlaSer 260
DB 337 ---GGGTATATAGCAATTAAAGTTTCACTGAGAAATAGAAATATATGAGTTCTCTTAAAGAA 304
QY 261 AlaArgIleAlaLysGluLeuGluLeuAspThrAlaThrIleGluValIleTyrLysGlu 280
DB 394 GACGCGATAGCAAAACAAATAGAAAAATGAAATAGAAATATATGAGTTCTCTTAAAGAA 453
QY 281 HisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIleProPheMet 300
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OM nucleotide nucleotide search, using SW model

Run on: January 16, 2003, 15:20:22 : Search time 59.2243 seconds
(without alignments)
16420.741 Million cell updates/sec

Query: US-09-026-459A-34
Perfect score: 4266
Sequences: 1 GATTAATAGTCTGCGGGAAT.....AAATAGCAATATGATGAT 4266

Scoring table: IDENTITY NUP
Gapop 10.0 : Gapext 1.0

Searches: 994868 seqs, 222944149 residues
Total number of hits satisfying chosen parameters: 787746

Minimum hit seq length: 0
Maximum hit seq length: 2000000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA:*

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- 2: /seqs/6/pdata/1/pubseq/0810_NEW_PUB.seq*
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- 9: /seqs/6/pdata/1/pubseq/0809_NEW_PUB.seq*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	Hit ID	Description
1	4266	100.0	4266	10 US-09-459-522-34	Sequence 34, Appl
2	4257	99.7	4324	10 US-09-469-522-32	Sequence 32, Appl
3	4257	99.7	4392	10 US-09-469-522-30	Sequence 30, Appl
4	4257	99.7	4455	10 US-09-469-522-28	Sequence 28, Appl
5	4257	99.7	4555	10 US-09-469-522-1	Sequence 1, Appl
6	4257	99.7	4839	9 US-09-954-531-143	Sequence 143, Appl
7	4253.8	99.6	4554	10 US-09-469-522-50	Sequence 50, Appl
8	4226	99.8	4324	10 US-09-469-522-38	Sequence 38, Appl
9	4225.4	99.8	4461	10 US-09-469-522-40	Sequence 40, Appl
10	4212	99.5	4218	10 US-09-469-522-3	Sequence 3, Appl
11	4107	99.1	4113	10 US-09-469-522-36	Sequence 36, Appl
12	4099	92.0	4447	10 US-09-469-522-42	Sequence 42, Appl
13	2898.6	88.8	4383	10 US-09-469-522-48	Sequence 48, Appl
14	2886.6	86.6	4377	10 US-09-469-522-45	Sequence 45, Appl
15	2827.4	86.6	4161	10 US-09-469-522-46	Sequence 46, Appl
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18	142.2	4.4	411	10 US-09-864-761-3141	Sequence 3141, Ap
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ALIGNMENTS

RESULT 1

US-09-469-522-34
Sequence 34, Applicant: US/09469522
Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji
Hu, Shi Xue
Benedito, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED KETIN-GLA-NOMA TUMOR SUPPRESSOR PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4434
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4434

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/469,522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Heller, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UIXC-506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
LENGTH: 3266 base pairs
TYPE: nucleic acid

Sequence 296, Appl
Sequence 37, Appl
Sequence 2546, Ap
Sequence 1, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 342, Appl
Sequence 344, Appl
Sequence 4, Appl
Sequence 11218, A
Sequence 14521, A
Sequence 4582, Ap
Sequence 154, Ap
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RESULT 13

US-09-469-522-48
Sequence 48, Application 05/04/95-22
Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji
Hu, Shi Xue
Benedict, William F.
Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR
PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

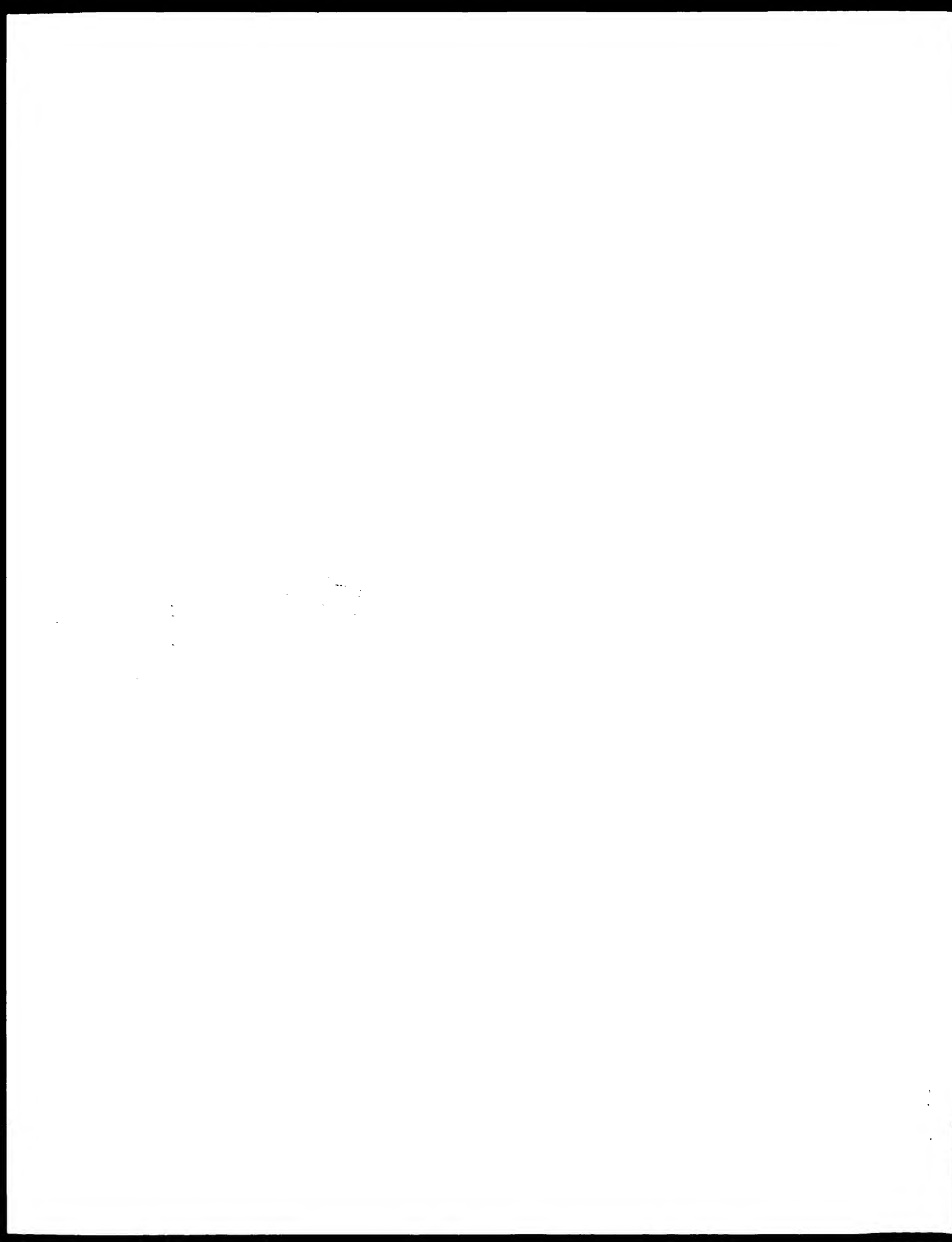
ADDRESSEE: Arnold, White & Durkee
STREET, P.O. Box 4433

1 NAME: Hiblot, David W.
2 REPLICATION NUMBER: 41,071
3 REFERENCE/LOCKER NUMBER: UTXC:506
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 512/418-3000
6 TELEFAX: 512/474-7577
7 INFORMATION FOR SEQ ID NO: 46:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 3477 base pairs
10 TYPE: nucleic acid
11 STRANDEDNESS: single
12 TOPOLOGY: linear
13 FEATURE:
14 NAME/KEY: CDS
15 LOCATION: 7..2613
16 SEQUENCE DESCRIPTION: N. SEQ ID NO. 46.

DS 09 469 522 46

Query Match 88.4% Score 2886.6; DB 10; Length 3377;
Best local similarity 94.4% Pred. No. 0.
Matches 4076; Conservative 0; Mismatches 4; Indels 177; Gaps 1;
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DB 1261 AATGACAACTATTCCTTATTTTAACTGACAGTGAATTCGAAAAAAGAGTATATGAAA 1320
QY 1210 TATGACAACTATTCCTTATTTTAACTGACAGTGAATTCGAAAAAAGAGTATATGAAA 1269
DB 1321 TATGACAACTATTCCTTATTTTAACTGACAGTGAATTCGAAAAAAGAGTATATGAAA 1380
QY 1270 CTAAATCTGATTCCTTATTTTAACTGACAGTGAATTCGAAAAAAGAGTATATGAAA 1329
DB 1381 CTAAATCTGATTCCTTATTTTAACTGACAGTGAATTCGAAAAAAGAGTATATGAAA 1440
QY 1330 GCAAGAGAGCAATAGCATACTATTTTAAAGACAAAATTTTAAAGACAAAATAGCATA 1389
DB 1441 GCAAGAGAGCAATAGCATACTATTTTAAAGACAAAATTTTAAAGACAAAATAGCATA 1500
QY 1390 ATGCAATCTGATTCCTTATTTTAACTGACAGTGAATTCGAAAAAAGAGTATATGAAA 1449
DB 1501 ATGCAATCTGATTCCTTATTTTAACTGACAGTGAATTCGAAAAAAGAGTATATGAAA 1560
QY 1450 GATGAGAGCAATAGCATACTATTTTAAAGACAAAATTTTAAAGACAAAATAGCATA 1509
DB 1561 GATGAGAGCAATAGCATACTATTTTAAAGACAAAATTTTAAAGACAAAATAGCATA 1620
QY 1510 AATGACAACTATTCCTTATTTTAACTGACAGTGAATTCGAAAAAAGAGTATATGAAA 1569
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QY 1570 TCAACTAGAGGAGTATGATTCCTTATTTTAACTGACAGTGAATTCGAAAAAAGAGTAT 1629
DB 1681 TCAACTAGAGGAGTATGATTCCTTATTTTAACTGACAGTGAATTCGAAAAAAGAGTAT 1740
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DB 1741 AGATGAGAGCAATAGCATACTATTTTAAAGACAAAATTTTAAAGACAAAATAGCATA 1800
QY 1690 GATGAGAGCAATAGCATACTATTTTAAAGACAAAATTTTAAAGACAAAATAGCATA 1749
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DB 1861 CATATGAGAGCAATAGCATACTATTTTAAAGACAAAATTTTAAAGACAAAATAGCATA 1920
QY 1810 AGATGAGAGCAATAGCATACTATTTTAAAGACAAAATTTTAAAGACAAAATAGCATA 1869
DB 1921 AGATGAGAGCAATAGCATACTATTTTAAAGACAAAATTTTAAAGACAAAATAGCATA 1980



PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459
 FILING DATE: UNKNOWN
 ATTORNEY/AGENT INFORMATION:
 NAME: HILBERT, DAVID W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UTIC:506
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:
 LENGTH: 3423 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

NAME/KEY: CUS

LOCATION: 7,12559

SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-09-469-522-42

Alignment Scores:

Prod. No.: 0 Length: 3423
 Score: 4372.00 Matches: 851
 Percent Similarity: 100.00% Conservativity: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-026-459a-33 (1-851) x US-09-469-522-32 (1-3423)

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 QY 21 LeuIrpGlyIleCysIlePheAlaValAspLeuAspGluMetSerPheThrPhe 40
 DB 67 CTGAGAGAAATGCTATGTTTATTGTAATGTTGATGATGATGATGATGATGATG 126
 QY 41 ThrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnLeuLysGlu 60
 DB 127 ACACAGCAGCAG 186
 QY 61 IleAspIleSerThrLysValAspAsnAlaMetSerArgLeuLysLysLysVal 80
 DB 187 ATGAG 246
 QY 81 LeuPheAlaIlePheSerLysLeuGluArgThrCysGlnLeuIleTyrLeuThrGlnPro 100
 DB 247 TGTGTGAG 306
 QY 101 SerSerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerIleThr 120
 DB 307 AGCAG 366
 QY 121 PheLeuLeuAlaLysGlyGluValLeuGlnMetGluAspLeuValIleSerPheGln 140
 DB 467 TTTTATTAGTAAAG 426
 QY 141 LeuMetLeuCysValLeuAspLysPheIleLysLeuSerProMetLeuLeuLysGlu 160
 DB 427 TTATGTATGTGCTGTGACTATTATTAACTATCAGCTCCAGTGCTGCTCAAGAGAA 486
 QY 161 ProTyrLysThrAlaValIlePheProIleAsnGlySerProArgThrProArgArgGlyGln 180
 DB 487 GCAATAG 546
 QY 181 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleIleValLeu 200
 DB 547 AACAG 606
 QY 201 CysLysGlnIleSerCysAsnIleAspLeuValLysAsnValLysPheLysAsnPheIle 220

DB 607 GTGAG 866
 QY 221 ProPheMetAspSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeu 240
 DB 667 GCTTATATGAGATGCTTGGAGCTTGTAAACATCTAAATGCACTTCCAGACCTTCAAAAAT 266
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 DB 727 TCTAAG 286
 QY 261 AspHisAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 280
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 QY 301 ValMetAsnThrIleGlnLeuMetMetIleLeuAsnSerAlaSerAspGluProSer 320
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 QY 321 GluAsnLeuIleSerIleAsnAsnGlyThrValAsnProLysGluSerIleLeuLys 340
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 DB 1087 TGTGTGAG 446
 QY 381 GluSerMetLeuLysSerGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeu 400
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 QY 401 AsnAspAsnIlePheHisMetSerLeuValGlyGlyAlaLeuValValMetAlaThr 420
 DB 1207 AATCAG 486
 QY 421 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheThrIle 440
 DB 1267 TATGAG 506
 QY 441 LeuAsnValLeuAsnLeuLysAlaPheAspPheLysValIleCysSerPheIleLys 460
 DB 1327 CTGAG 526
 QY 461 AlaGlyGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGlnHisArgIle 480
 DB 1487 GCAAG 546
 QY 481 MetGluSerLeuAlaIlePheLeuSerAspSerProIlePheAspLeuLysGlnLys 500
 DB 1447 ATGAG 566
 QY 501 AspArgGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProGln 520
 DB 1507 GAG 586
 QY 521 AsnAsnIleThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLys 606
 DB 1567 AATAAACAG 626
 QY 541 SerIleThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaIleGln 560
 DB 1627 TCAATAG 626
 QY 561 ThrGlnLysProLysSerThrSerLeuSerLeuPheIleTyrLysLysValLysArgLeu 580

142 MetLeuValLeuAspThrPheIleLysLeuSerProMetLeuLeuLysGluPro 161
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RESULT 3
ms-09-469 522-28

1 Sequence 28, Application US/09469522
 2 Patent No. US200201441A1
 3 GENERAL INFORMATION:
 4 APPLICANT: XU, Hong Ji
 5 RO, Shi Xue
 6 Inventor: William F
 7 Zhou, Yunli
 8 TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
 9 PROTEINS
 10 NUMBER OF SEQUENCES: 51
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: Arnold, White & Burke
 13 STREET: P.O. Box 4433
 14 CITY: Houston
 15 STATE: TX
 16 COUNTRY: USA
 17 ZIP: 77210 4433
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: Floppy disk
 20 COMPUTER: IBM PC compatible
 21 OPERATING SYSTEM: MS DOS/MS DOS
 22 SOFTWARE: Patent In Release #1.0, Version #1.40
 23 CURRENT APPLICATION DATA:
 24 APPLICATION NUMBER: US/95/345,522
 25 FILING DATE: 22 Dec 1999
 26 CLASSIFICATION: Unknown
 27 PRIOR APPLICATION DATA:
 28 APPLICATION NUMBER: 09/026,459
 29 FILING DATE: Unknown
 30 ATTORNEY/AGENT INFORMATION:
 31 NAME: Heller, David W.
 32 REGISTRATION NUMBER: 41,071
 33 REFERENCE/PACKET NUMBER: US/506
 34 TELEPHONE: 512/474 3000
 35 TELEFAX: 512/474 7577
 36 INFORMATION FOR SEQ ID NO: 28:
 37 SEQUENCE CHARACTERISTICS:
 38 LENGTH: 3455 base pairs
 39 TYPE: nucleic acid
 40 SUBSTANCE: single
 41 TOPOLOGY: linear
 42 FEATURE:
 43 NAME/KEY: CUS
 44 LOCATION: 7..2691
 45 SEQUENCE DESCRIPTION: SEQ ID NO: 28:
 46 US 09 469 522 28
 47 Alignment Scores:
 48 Prod. No.: 0 Length: 3455
 49 Scores: 4667.00 Matches: 850
 50 Percent Similarity: 100.00% Conservativity: 0
 51 Best Local Similarity: 100.00% Mismatches: 0
 52 Query Match: 99.83% Indels: 0
 53 Gaps: 10
 54 US 09 026 459a 33 (1 853) x US 09 469 522 28 (1 3455)
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 60 22 TTTTCT 41
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 62 202 TGGGAACTCTGATGATGATGATGATGATGATGATGATGATGATGATG 261
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 68 62 AspThrSerThrLysValAspAsnAlaMetSerAlaLeuLeuTyrAspVal 81
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 70 322 GATACAG 381

82 PheValLeuPheSerLysLeuGlnArgThrCysGlnLeuTleTyrLeuThrGlnProSer 101
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 84 382 TTTGGACCTCTGAGTAAATTCGAAAGGACATCTGAAATTAATAATATGAAATACAT 441
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 86 102 SerSerTleSerThrLeuLeuAsnSerAlaLeuValLeuGlnValSerTyrTleThrPhe 121
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 88 442 AHTTGATATATATCTGAAATAAATTTGCTATGAGTGTGAAAGATTTCTTCTGATTA 501
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 90 122 LeuLeuAlaTyrGlyCysLeuValLeuGlnMetGlnAspAspGlnValTleSerPheGln 141
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 92 502 TTATTAGCTTAAAGGGGAGATTTACAAATGAGAGATGATGAGATTTGTTGATTTA 561
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 100 622 TATAAAGAGCTGTTATATCTATTAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 681
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 102 182 ArgSerAlaArgTleAlaTyrGlnTleLeuTleAsnAspThrArgTleTleValValLeuPys 201
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 106 202 LysGlnLysGlnCysAsnTleAspGlnValTyrAsnValTyrPheGlnAsnPheTyrPro 221
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 108 742 AAAGAACATGAAATGATTAATACAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 801
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 112 802 TTTATGATTTCTTGGACTGTGATGATGATGATGATGATGATGATGATGATGATGAT 861
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 128 1042 ATGACACACTATGCAACAAATTAATGATGATTTTAAATTCAGTAAATGATGATGATG 1101
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 130 322 AsnLeuTleSerTyrPheAsnArgCysThrValAsnProGlnGlnSerTleLeuLysArg 341
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 132 1102 AATCTGATTTCTTATTAACAACTGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1161
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 152 1402 ASCAGAAATATATCTCAAAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1461

442 AsuValLeuAsnLeuThrAlaPheAspPheTyrLysValIleGluSerPheIleLysAla 461
1462 AATGGCTTAAATTAAGAGCTGTTGATTTACAAAGGATGATGAAAGCTTTATCAACAGCA 1521
462 GluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMet 481
1522 GAAGGCAATTTGAAAGCAATTAATAAATATTAGAACGATGTAAATGCAATCATG 1581
482 GluSerIleAlaIlePheLeuSerProLeuPheAspLeuIleLysGluSerLysAsp 501
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1702 AATGCAATGTCAGTAT 1761
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1762 ACTAGCGTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1821
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622 HisThrArgGlnIleAsnMetCysSerMetTyrThrLysValLysAspLeuAsp 641
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642 LeuThrPheLysThrGluValThrAlaThrLysAspLeuProHisAlaValGluThr 661
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662 PheLysArgValLeuIleLysGluGluGluThrAspSerIleLeuValPheTyrAsnSer 681
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682 ValPheMetGluArgLeuLysThrAsnIleLeuThrTyrAlaSerThrArgProPheThr 701
2182 GCT 2241
702 LeuSerProIlePheGluArgSerProTyrLysPheProSerProLysArg 721
2242 TATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2301
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782 LeuLysArgSerAlaGluThrSerAsnProIleLysTyrCysLysLysLeuArgPheAsp 801
2482 CCAAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2541
802 ThrThrLysSerAspThrAlaAspGlySerLysHisLeuProGlyGluSerPheGln 821

2542 ATTCAAGCATAGATGAGTACATGAGTAAATATCTCCAGAGAGATGCAAAATTTCA 2601
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RESULT 4
US-09-469-522-1
Sequence 1, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RHINOBLASTOMA TUMOR SUPPRESSOR PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, version #1.30
CURRENT APPLICATION DATA:
AFFILIATION NUMBER: US-09-469-522
FILING DATE: 22-Dec-1999
CLASSIFICATION: C06K40
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTXC-506
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3555 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2790
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-469-522-1
Alignment Scores:
Pred. No.: 0 Length: 4555
Score: 4367.00 Matches: 850
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 10 Gaps: 0
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442 AsnValLeuAsnLeuGlySerGlyThrAspLeuSerPheProIleLeu 461
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1752 GAAGGCAATCTCACAACAACAAAGATTAAGACCAAGTCAACATCAATCAATG 1811
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522 AsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysGlySer 541
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2712 CTCAAAAGAGTCTGAAAG 2771
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842 SerMetAspThrSerAsnLysGluGluLys 851
2892 AGCATGATACCTCAAAAG 2941

RESULT 6

US-09-860-211-7
Sequence 7, Application US/09860211
Patent No. US2002014721A1
GENERAL INFORMATION:
APPLICANT: Gregory, Richard J.
Willis, Ken N.
Maneval, Daniel C.
TITLE OF INVENTION: Recombinant Adenoviral Vector and Methods of Use
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/860,211
FILING DATE: 18-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/328,673
FILING DATE: 15-FEB-2000
APPLICATION NUMBER: US 08/142,669
FILING DATE: 25-OCT-1993
APPLICATION NUMBER: US 08/233,669
FILING DATE: 26-APR 1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy S.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 016930-00092005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2995 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 139..2925
OTHER INFORMATION: /product= "KH"
/note= "relinblastoma tumor suppressor"
SEQUENCE DESCRIPTION: SEQ ID No: 7:
US-09-860-211-7
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 QY 462 GluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMet 481
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 QY 482 GluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAsp 501
 DB 1504 SAATGCTTTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1563
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 DB 1624 AATGACAATGAGAGAGATATATATCTTCTGCTGATGCTGATGCTGATGCTGATGCTGAT 1683
 QY 542 ThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThr 561
 DB 1684 ACTAGGCTGTGTAATATCTGAG 1743
 QY 562 GluLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAla 581
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 QY 602 ThrThrThrPhePhePheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArg 621
 DB 1864 AICATCTGAG 1923
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 QY 642 LeuLysPheLysIleIleValThrAlaLysLysAspLeuProHisAlaValGlnGlnThr 661
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 DB 2104 GCTCTCATCCAG 2163
 QY 702 LeuSerProThrProHisIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 721
 DB 2164 TTGTCAGAAATACATCTGCTGAG 2223
 QY 722 ProProGlyGlyAsnIleLysSerProLeuLysSerProLysLysLysLysLysLysLys 741
 DB 2224 ATCTGAG 2283
 QY 742 LeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSer 761
 DB 2284 GTGCGAATACCAACAAAG 2343

QY 762 PheGlyThrSerGlyLysPheGlnLysIleAsnGlnMetValCysAsnSerAspAlaVal 781
 DB 2344 TTGCGAATACCAACAAAG 2403
 QY 782 LeuLysArgSerAlaGluGlySerAsnProPheLysPheLeuLysLysLysLysLysLys 801
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 DB 2464 ATTAAGAGATATATTAAGAGATATATTAAGAGATATATTAAGAGATATATTAAGAGATAT 2523
 QY 822 GluLysLeuAlaGluMetIleThrSerThrArgThrArgGlnClnLysGlnLysMetAsnAsp 841
 DB 2524 CAG 2583
 QY 842 SerMetAspThrSerAsnLysGlnGlnLys 851
 DB 2584 AGCATGATACCTCAACAG 2643
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 US-09-469-522-48
 : Sequence 48, Application US/09469522
 : Patent No. US20020151461A1
 : GENERAL INFORMATION:
 : APPLICANT: Xu, Hong-Ji
 : Hu, Shi-Xue
 : Benedict, William F.
 : Zhou, Yunli
 : TITLE OF INVENTION: MODIFIED REINOHLASIOMA TUMOR SUPPRESSOR
 : PROTEINS
 : NUMBER OF SEQUENCES: 51
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Arnold, White & Durkee
 : STREET: P.O. Box 4433
 : CITY: Houston
 : STATE: TX
 : COUNTRY: USA
 : ZIP: 77210-4433
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09469,522
 : FILING DATE: 22-Dec-1999
 : CLASSIFICATION: <Unknown>
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 09/026,459
 : FILING DATE: <Unknown>
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Hibler, David W.
 : REGISTRATION NUMBER: 41,071
 : REFERENCE/DOCKET NUMBER: UICX:506
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 512/418-3000
 : TELEFAX: 512/474-7577
 : INFORMATION FOR SEQ ID NO: 48:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 3383 base pairs
 : SYL: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 7..2619
 : SEQUENCE DESCRIPTION: SEQ ID NO: 48:
 US-09-469-522-48
 Alignment Scores:
 Pred. No.: 0 Length: 3383
 Score: 4017.50 Matches: 793

[illegible]

SEQUENCE CHARACTERISTICS:

LENGTH: 3447 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

FEATURES:

NAME/KEY: CDS
 LOCATION: 7..2583
 SEQUENCE DESCRIPTION: SEQ ID NO: 42

US 09-026 459A-33 (1-851) x US-09-459-522-42 (1-3347)

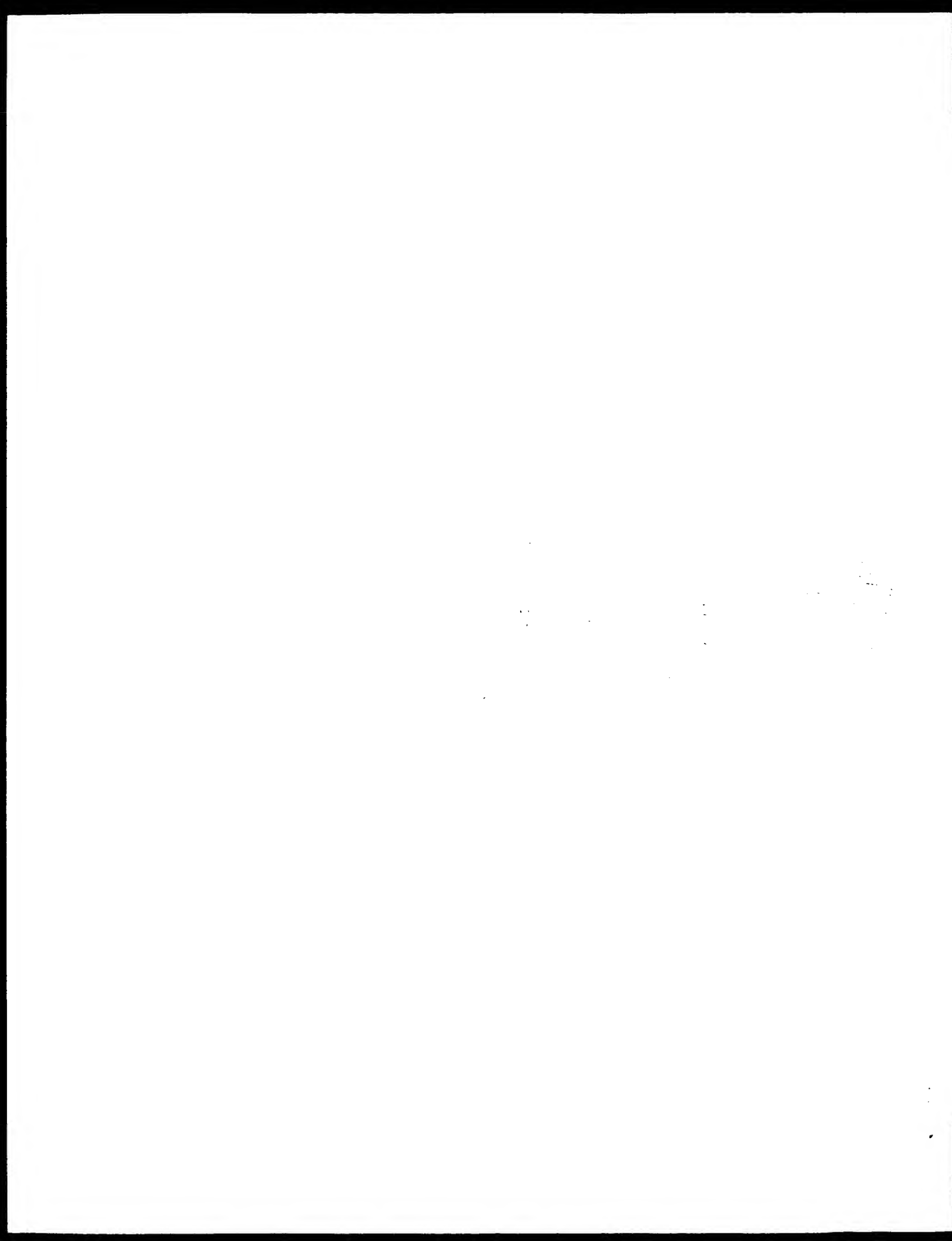
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 Score: 3971.50 Matches: 780
 Percent Similarity: 91.76% Conservative: 0
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 Query Match: 90.84% Indels: 69
 Gaps: 1

US 09-026 459A-33 (1-851) x US-09-459-522-42 (1-3347)

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 02 241 GAGAAAGTTTATGTCGTGAGAGAGATATTTGAGAGTTATATTTAAAAAAGAAATG 400
 03 22 TrpGlyIleCysIlePheIleAlaValAspLeuAspGluMetSerPheThr 41
 04 10035AAATCTGATCTTATTCAGGACATTCACCTACTCGAA----- 342
 05 42 GluLeuGlnLysAsnIleGluSerValHisLysPheAsnLeuLeuLysGluIle 61
 06 42 ----- 342
 07 62 AspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysIleValAspVal 81
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 12 104 ITATTAGCTAAAGAGAAATATTAAATGAAAGATGATGATGATGATGATGATGATGAT 453
 13 142 MetLeuLysValLeuAspTyrPheIleLysLeuSerProPheMetLeuLeuLys 161
 14 154 AGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 513
 15 162 TyrLysThrAlaValIlePheProLysAsnGlySerProMetThrProArgArg 181
 16 174 TATATAAAATAGTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 573
 17 182 ArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleLeuGluVal 201
 18 174 AGGATGAGAGAGATAGAGAAATATATATAAATATATATAAATATATATAAATATAT 633
 19 202 TyrThrGlnIleGlyAsnValIleAspValTyrPheLysAsnIlePro 221
 20 174 AAAAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAAT 693
 21 222 PheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsn 241
 22 174 ITTATGAATTCCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
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 32 1534 CGAAGAGCAATATATATATTTGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1593
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 34 1594 AATCAAT 1653
 35 542 ThrThrArgValAsnSerThrAlaAsnAlaGluThrGluAlaThrSerAlaThr 561
 36 1654 ACTACCGCTGTAAT 1713
 37 562 GlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 581
 38 1714 CAGAGCAATATGAAAT 1773
 39 582 TyrLeuArgLeuAsnThrLeuGlySerGlnArgLeuSerGlnHisProGlnLeuHis 601
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 42 1834 ATCATCTGAGCTTTTTCAGACACCTGCTGAGATATATATATATATATATATATAT 1893
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Genome version 5.1.3
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Run on: January 16, 2003, 15:20:22 : Search time 9.7916 seconds
(without alignments)
16320.741 Million cell updates/sec

Query: US-09-026-459A-32

Perfect score: 3425

Sequence: 1 GCAATGAGGAGAAATTTG.....AAATGAGATTAATGATAGT 3425

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searches: 69068 seqs, 22294149 residues

Total number of hits satisfying chosen parameters: 78776

Minimum hit seq length: 6

Maximum hit seq length: 2000000

Post processing: Minimum Match 6%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA:

- 1: US-09-026-459A-32 (pubseq) US-09-026-459A-32 seq
- 2: US-09-026-459A-32 (pubseq) US-09-026-459A-32 seq
- 3: US-09-026-459A-32 (pubseq) US-09-026-459A-32 seq
- 4: US-09-026-459A-32 (pubseq) US-09-026-459A-32 seq
- 5: US-09-026-459A-32 (pubseq) US-09-026-459A-32 seq
- 6: US-09-026-459A-32 (pubseq) US-09-026-459A-32 seq
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- 12: US-09-026-459A-32 (pubseq) US-09-026-459A-32 seq
- 13: US-09-026-459A-32 (pubseq) US-09-026-459A-32 seq
- 14: US-09-026-459A-32 (pubseq) US-09-026-459A-32 seq

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3415	99.8	3492	10	US-09-459-522-30	Sequence 30, Appl
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4	3415	99.8	3555	10	US-09-459-522-1	Sequence 1, Appl
5	3415	99.8	4839	9	US-09-954-531-143	Sequence 143, Appl
6	3411.8	99.7	4554	10	US-09-459-522-45	Sequence 50, Appl
7	3407	98.0	3266	10	US-09-459-522-34	Sequence 34, Appl
8	3406	97.1	3324	10	US-09-459-522-48	Sequence 38, Appl
9	3425.4	97.1	3461	10	US-09-459-522-40	Sequence 40, Appl
10	3422	96.7	3218	10	US-09-459-522-46	Sequence 3, Appl
11	4107	94.5	3114	10	US-09-459-522-46	Sequence 36, Appl
12	3006	90.5	3447	10	US-09-459-522-42	Sequence 42, Appl
13	2956.6	89.0	3483	10	US-09-459-522-48	Sequence 48, Appl
14	2944.5	88.5	3472	10	US-09-459-522-45	Sequence 46, Appl
15	2827.4	85.1	3161	10	US-09-459-522-44	Sequence 44, Appl
16	2618.4	78.8	2995	10	US-09-860-211-7	Sequence 7, Appl
17	428	12.9	451	9	US-09-796-692-7740	Sequence 7740, Ap
18	142.2	4.3	411	10	US-09-864-761-3141	Sequence 3141, Ap
19	129	3.9	129	10	US-09-864-761-19910	Sequence 19910, A

20	104	3.1	304	10	US-09-964-824A-296	Sequence 296, Ap
21	48.8	2.1	3960	9	US-09-292-758-47	Sequence 47, Appl
22	59.4	1.8	324	9	US-09-796-692-2546	Sequence 2546, Ap
23	51	1.5	4747	10	US-09-770-657-1	Sequence 1, Appl
24	51	1.5	4747	12	US-10-925-676-2	Sequence 2, Appl
25	49.4	1.5	640681	10	US-09-790-988-1	Sequence 1, Appl
26	48.8	1.5	33513	9	US-09-754-853A-2	Sequence 2, Appl
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28	48.4	1.5	419	10	US-09-969-473-44	Sequence 44, Appl
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31	47.8	1.4	424	10	US-09-960-352-11218	Sequence 11218, A
32	47.6	1.4	411	10	US-09-960-352-11521	Sequence 11521, A
33	47	1.4	393	10	US-09-960-352-4582	Sequence 4582, Ap
34	46.2	1.4	302250	10	US-09-962-832-154	Sequence 154, Ap
35	45.8	1.4	431	10	US-09-960-352-5598	Sequence 5598, Ap
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37	45.4	1.4	516	10	US-09-960-352-5785	Sequence 5785, Ap
38	45.2	1.4	640681	10	US-09-790-988-1	Sequence 1, Appl
39	44.6	1.3	555	10	US-09-864-761-12458	Sequence 12458, A
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41	44.6	1.3	2000	9	US-09-948-842A-4147	Sequence 4147, Ap
42	44.4	1.3	2000	9	US-09-948-842A-4050	Sequence 4050, Ap
43	44.2	1.3	1376	10	US-09-970-927A-749	Sequence 749, Ap
44	44.2	1.3	2000	9	US-09-948-842A-5166	Sequence 5166, Ap
45	44.2	1.3	1299	10	US-09-220-091-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-459-522-32

Sequence 32, Applicant: US-09-459-522

Patent No. US-20151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Burke

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-09-459-522

FILING DATE: 22-Dec-1999

CLASSIFICATION: Unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: Unknown

ATTORNEY/AGENT INFORMATION:

NAME: Hilbert, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UIXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 342 base pairs

TYPE: nucleic acid

GENERAL INFORMATION:

APPLICANT: Xu, Hong-di
Hu, Shi-xue
Houdict, William F.
Zhao, Yunli

TITLE OF INVENTION: MODIFIED RETINORASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
SURREY, P.O. Box 4433
CITY: Houston
STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: 22 Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: DTXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 3377 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME: KEY: ITS

LOCATION: 7..2614

SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US 09 469 522-46

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Best Local Similarity 94.5%, Pred. No. G.

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File: us-09-026-459a-31

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Searched: 30868 seqs, 2294149 residues

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Minimum DB seq length: 0

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Post processing: Minimum Match 0%

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Listing first 4% summaries

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	4499	99.9	445	10	US-09-469-522-28 Sequence 28, Appl
3	4499	99.9	455	10	US-09-469-522-3 Sequence 1, Appl
4	4499	99.9	489	9	US-09-954-631-143 Sequence 143, App

5	4489	99.7	2995	10	US-09-860-211-7 Sequence 7, Appl
6	4489	99.7	3554	10	US-09-469-522-50 Sequence 50, Appl
7	4367	97.0	3423	10	US-09-469-522-42 Sequence 42, Appl
8	4307	95.6	3461	10	US-09-469-522-40 Sequence 40, Appl
9	4273	94.9	3266	10	US-09-469-522-34 Sequence 34, Appl
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ALIGNMENTS

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Sequence 30, Application US/09469522
Patent No. US20020150461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong Ji
Hu, Shi-Xue
Benodiet, William F.
Zhao, Yunli

TITLE OF INVENTION: MODIFIED PBTIN-BLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Burke

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210 4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09469522

FILING DATE: 22-Dec 1999

CLASSIFICATION: <Unknown>


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08-09-469-522-28
 Sequence 28, Application US-09-469-522

Patent No. US-2002-015346-1A1
 GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ti
 Hu, Shi Xue
 Hemdick, William F.
 Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR
 PROTEINS

NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Burke
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210-4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.40
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09-469-522
 FILING DATE: 22 Dec 1999
 CLASSIFICATION: Unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/026,459
 FILING DATE: Unknown
 ATTORNEY/AGENT INFORMATION:
 NAME: Hiblot, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: UTX-506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-4000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 28:
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 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
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 NAME/KEY: CDS
 LOCATION: 7..2491
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 162 PheGlnLeuMetLeuLysValLeuAspPyrPheIleLysLeuSerProProMetLeuLeu 181
 163 TTTACGTTAAAGCTATGCTGCTGATATTTATTAACATTCCTACCTGCTGCTGCTGCTG 612
 182 LysGlnProTyrLysThrAlaValIleProIleAsnGlySerProArgProArgArg 201
 183 AAACAAATCATATAAAACATGTTGTTATACCTATTAATGCTTACCTGCTGCTGCTGCTG 672
 202 GlyThrAspArgSerAlaAlaGluLeuLysGlnLeuGluAsnAspThrArgIleIleGlu 221
 203 GGTGCAAAATAGAGATGTAAGATGTAAGATGTAAGATGTAAGATGTAAGATGTAAGATG 732
 222 ValLeuAspLysThrGluLysAsnIleAspGluValLysAsnValIlePheLysAsn 241
 243 GTTCTCTTAAACAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 792
 242 PheIleProPheMetAsnSerLeuGlyLeuValThrSerAspGlyLeuProGluValGlu 261
 263 TTTAAGCTTTTATCAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 852
 262 AspLeuSerLysArgPheGluGluIlePheLysGluLysAsnLysAspAlaArgLeu 281
 283 AATCTTCTTAAGCATATGAAAGAAATTTATCTTAAATATTAAGATCTAGATCAAGATTA 912
 282 PheLeuAspHisAspLysThrGluGlnThrAspSerIleAspSerPheGluThrGlnArg 301
 303 TTTTGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 972
 302 ThrProSerLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProVal 321
 323 ACACCAAGAAAGATCACTTGAAGAGAGGTAATGTAATGTAATGTAATGTAATGTAATG 1032
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 343 AGACTGTTATGAACATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1092
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 362 LeuLysValValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysValValGly 381
 383 CTCAAAAGATGAGAGATATAGATATGATATGATATGATATGATATGATATGATATG 1212
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 423 GTTAAAGAAATGCTTAAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1332
 422 LeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaLysAlaLeuGluValValMet 441
 443 CTCTGCAAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1392
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 463 AT 1452
 462 ThrIleLeuAsnValLeuAsnLeuLysAlaPheAspPheLysValIleIleGluSerPhe 481
 483 TGAATCTGAAGTCTGTTAATTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1512
 482 IleLysAlaGluLysAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHis 501

1513 ATCAAAACATCAAGGCAACTTGCACAGAGAAATGATAAACATTTTAAAGATGTCGAAAT 1572
 502 ArgIleMetGluSerLeuAlaIlePheLeuSerAspSerProLeuPheAspLeuIleLysHis 521
 523 CGAATCAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1632
 522 SerLysAspArgGlyGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuPro 541
 543 TCAAGGCAATGCAAGGCAATGCAAGGCAATGCAAGGCAATGCAAGGCAATGCAAGGCA 1692
 542 LeuGluAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLys 561
 563 CTCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1752
 562 LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 581
 583 AAAGGTTTAAATGAGGTTTAAATGAGGTTTAAATGAGGTTTAAATGAGGTTTAAATG 1812
 582 PheGlnThrGlnLysProLysSerThrSerLeuSerLeuPheTyrLysLysValTyr 601
 603 TTTCAAGGCAATGCAAGGCAATGCAAGGCAATGCAAGGCAATGCAAGGCAATGCAAG 1872
 602 ArgLeuAlaTyrLeuArgLeuAsnThrLeuGlyGluArgLeuLeuSerGluHisProGlu 621
 623 CGGTAT 1932
 622 LeuGluHisIleIleIleThrPheGluHisThrLeuGluAsnGluThrGluLeuMet 641
 643 TTAT 1992
 642 ArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyLysCysLysValLys 661
 663 ACACACAGGCAATGCAAGGCAATGCAAGGCAATGCAAGGCAATGCAAGGCAATGCAAG 2052
 662 AsnIleAspLeuLysPheLysIleIleValThrAlaThrLysAspLeuPheHisAlaVal 681
 683 AT 2112
 682 GluGluThrPheLysArgValIleLysGluGluGlyTyrAspSerIleIleValPhe 701
 703 AT 2172
 702 TyrAsnSerValPheMetGluArgLeuLysThrAsnIleLeuGluIleTyrAlaSerThrArg 721
 723 TATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2232
 722 ProProThrLeuSerProIleProHisIleProArgSerProTyrLysPhePheSerSer 741
 743 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2292
 742 ProLeuArgIleProGlyLysAsnIleGlyTyrIleSerPheLysSerProTyrLysHis 761
 763 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2352
 762 SerGluGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIle 781
 783 TCAAGGCAATGCAAGGCAATGCAAGGCAATGCAAGGCAATGCAAGGCAATGCAAGG 2412
 782 GlyGluSerPheGlyThrSerGluLysPheGluLysIleAsnGluMetValLysAsnSer 801
 803 GTTAAAT 2472
 802 AspArgValIleLysArgSerAlaGluGlySerAsnProThrLysProLeuLysLysLys 821
 823 AT 2532
 822 ArgPheAspIleGluLysSerAspGluAlaAspGlySerLysHisIleuProGluLysLys 841
 843 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2592
 842 LysPheGluGluLysLeuAlaGluMetThrSerThrArgMetGluLysLysLysLys 861

140 2553 AATATTAGAGAAATTTAGAAATTAATTTACTTTCAGAACAGAAATGAAAGAGAGAA 2652.

57 862 MetAspSerMetAspThrSerAsnLysGlnGlnLys 874

140 2653 AATGAAATCAATATGCAATCAAAATCAAGAAAGAGAGAA 2691

RESULT 1

US 09 469 522 1

Sequence 1, Application US/09/469522

Patent No. US20020151461A1

GENERAL INFORMATION:

Applicant: Xu, Huiji

Attorney/Agent: Xu, Huiji

Inventor: Xu, Huiji

Address: 400, Box 4433

City: Houston

State: TX

Country: USA

Zip: 77210 4433

Medium Type: Floppy disk

Operating System: IBM PC compatible

Software: Patent In Release #1.0, Version #1.40

Current Application Data:

Application Number: US 09 469 522

Filing Date: 22 Dec 1999

Classification: unknown

Prior Application Data:

Application Number: 09/026,459

Filing Date: unknown

Attorney/Agent Information:

Name: Huiji Xu, David W.

Registration Number: 41,071

Reference/Check Number: UIX0506

Telecommunication Information:

Telephone: 512/418 5000

Telefax: 512/474 3577

Information For Seq ID No: 1:

Sequence Characteristics:

Length: 4555 base pairs

Type: nucleic acid

Strand: single

Topology: linear

Flatture:

Name/Key: CUS

Location: 7..2790

Sequence Description: SEQ ID NO: 1:

US 09 469 522 1

Alignment Scores:

Prod. No.: 0

Length: 4555

Matches: 878

Conservation: 0

Mismatches: 0

Indels: 0

Gaps: 0

US 09 026 459a 31 (1-874) x US 09 469 522-1 (1-3555)

57 2 AspPheThrAlaLeuPheSerValIlePheAspHisValArgGlnArqAlaTrp 21

140 172 GATTTTACGCAATATGCAAGAAATTAAGATACCACATCACTCAGACAGAGAGCTTGG 231

57 22 LeuThrTrpGlnLysValIlePheSerValIlePheGlyValIleGlnLysLys 41

140 242 TTAAATTGGAGAAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 291

42 LysGlnLeuTrpGlnLysValIlePheSerValIlePheAspHisValArgGlnArqAlaTrp 61
140 292 AAGCAACGTCGCGGAACTGCTATCTTATTCAGACACACACACACACACACACACACACAC 451
57 62 ThrPheThrGlnLeuGlnLysAsnLysValIlePheSerValIlePheGlyValIleGlnLys 81
140 352 ACTTTTACTGAGTACAGAAAAATAGAAATCATGTCGCAATAAATCTTAAATTAATA 411
57 82 LysGlnLeuAspThrSerThrLysValIlePheSerValIlePheGlyValIleGlnLysLys 101
140 412 AAGAAATGATACGAGTACCAAGTTGATATGTCATGTCAGACGTCGTCAGAGAGAGAT 471
57 102 AspValLeuPheAlaLeuPheSerLysLeuGlnArqThrCysGlnLeuLysLysLys 121
140 472 GATGATATGTCGACCTTCACCAAAATTCGAAAGACACATGACATTAATAATA 531
57 122 GlnProSerSerLysThrGlnLeuLeuAsnSerValIlePheSerValIleGlnLysValSerTrp 141
140 532 CAGCCAGCAGTTGATATGTCATGAAATTAATTCGTCATTCGTCATTCGTCATTCGTCATTCG 591
57 142 IleThrPheLeuLeuAlaLysGlyGlnValIleGlnLeuMetGlnAspSerValIleSer 161
140 592 ATCAATTTTATTAATTAAGGGGAGATTAATAAAGAAATTAATAATAATAATAATAATA 651
57 162 PheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeu 181
140 652 TTCAGTTAAATGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 711
57 182 LysGlnProTyrLysThrAlaValIlePheGlnLeuAsnLysSerProArqThrArqAla 201
140 712 AAGAACCTATTAAGACAGTGGTTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 771
57 202 GlyCysAsnArgSerAlaArgLeuAlaLysGlnLeuLeuGlnLeuAsnAspSerValIle 221
140 772 GGTGAGAACAGGAGTGCAGATAGCAACCACTAGCAACCACTAGCAACCACTAGCAACCACT 831
57 222 ValLeuCysLysGlnLeuThrCysAsnLysAspLysValIlePheSerValIlePheSerVal 241
140 832 GTTCTGCTGTAAGCAACATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 891
57 242 PheIleProPheMetAsnSerLeuGlnLeuValIlePheSerValIlePheSerValIlePhe 261
140 892 TTTATACCTTTTATGAAATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 951
57 262 AsnLeuSerLysArgTyrGlnGlnLysLysLysLysLysLysLysLysLysLysLysLys 281
140 952 AATCTTTTAAAGCAACAGAAAGAAATTTATCTTAAAGCAACAGAAATTTATCTTAAAGCA 1011
57 282 PheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSerPhePheThrThrGlnArq 301
140 1012 TTTTGGATGATGATAAAACCTTCACACGATGATGATGATGATGATGATGATGATGATGAT 1071
57 302 ThrProArgLysSerAsnLeuAspGlnGlnValIlePheProPheIleProPheIleProVal 321
140 1072 ACACAGCAAGAAAGTAACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1131
57 322 ArgThrValMetAsnThrIleGlnGlnLeuMetMetIleLeuAspSerAlaSerAspHis 341
140 1132 AGCACTGTTATGACACATATGCAACCAATTAATGATGATTTTAAATTTAAATTTAAATTTAA 1191
57 342 ProSerGlnAsnLeuIleSerTyrPheAsnAsnLysThrValIleProLysGlnSerIle 361
140 1192 CCTTCAGAAAAATGATTTGCTATTTTAAACACAGACAGACAGACAGACAGACAGACAG 1251
57 362 LeuLysArgValLysAspIleGlyTyrIlePheLysLysLysLysLysLysLysLysLys 381
140 1252 CTGAAAG 1311
57 382 GlnGlyCysValGlnLeuLysSerGlnArqTyrLysLysLysLysLysLysLysLysLys 401
140 1312 CAGGGTGTGCGAAATTTGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1371

QY 442 AlaThrTyrSerArgSerThrSerglnAsnLeuAspSerTgylThrAspLeuSerPhePro 461
 DB 1499 GGCACATATACACAGACATCAGCAAACTTGTGATCTGGACACACATCTGCTCTCCCA 1458
 QY 462 TrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPhe 481
 DB 1454 TGGATCTGTAATGCTTAATTTAAAAGCGTTTGGATTTTACAAAGTGATCGAAGATTTT 1518
 QY 482 CileysAlaGluGlyAsnSerThrArgGluMetIleCysHisGluGluArgCysGluHis 501
 DB 1519 ATCAAAAGCAAGAGCAATTTGCAAAAGCAATGATTAATTAATTTAGAGGATGTGAACAT 1578
 QY 502 ArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGln 521
 DB 1579 GCAATCAAGCAATCCCTGCAAGCAATGCAAGCAATCAAGCAATCAAGCAATCAAGCAAT 1638
 QY 522 SerTyrAspArgGluGlyProThrAspHisLeuGluSerAlaTyrProLeuAsnLeuPhe 541
 DB 1639 TCAAGGACGCAAGAGCAATTTGATTAATTTGATTAATTTGATTAATTTGATTAATTT 1598
 QY 542 LeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLys 561
 DB 1699 CTCAGATATATAC 1758
 QY 562 LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGluAlaThrSerAla 581
 DB 1759 AAAGCTTCAAAACAGCGTGAAATCTACGCAAAATGCCACACACACACACACACACAC 1818
 QY 582 PheGlnThrGlnLysPheLeuLysSerThrSerLeuSerLeuPheTyrLysValTyr 601
 DB 1819 TTAAGAGCAAGCAAGCAATTTGATTAATTTGATTAATTTGATTAATTTGATTAATTT 1878
 QY 602 ArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGlu 621
 DB 1879 GAGGTAGCTATCTCGGCAATTAATAATTTGATTAATTTGATTAATTTGATTAATTT 1938
 QY 622 LeuGluHisIleIleThrLeuPheGlnIleThrLeuGlnAsnGluTyrGlnLeuMet 641
 DB 1939 TTAAGCAATCAATCTGCAAGCAATTTGCAAGCAATTTGCAAGCAATTTGCAAGCAAT 1998
 QY 642 ArgAspAlaIleLeuAspSerIleLeuMetMetCysAspMetTyrGluLysValLys 661
 DB 1999 AGAAGCAAGCAATTTGATTAATTTGATTAATTTGATTAATTTGATTAATTT 2058
 QY 662 AsnGlnAspGluLysPheLysValThrAlaTyrIleAspLeuProHisAlaVal 681
 DB 2059 AATATAGCTTAATTTCAAAATCAATTTGATTAATTTGATTAATTTGATTAATTT 2118
 QY 682 GluThrThrPheCysArgValLeuIleLysGluGluGlyTyrAspSerIleIleValPhe 701
 DB 2119 CAGACATATATCAAGCAATTTGCAAGCAATTTGCAAGCAATTTGCAAGCAATTTGCA 2178
 QY 702 TyrAspSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArg 721
 DB 2179 TATACTGCTGCTAT 2238
 QY 722 ProThrThrLeuSerProIleProHisIleProArgSerProTyrLysPheProSer 741
 DB 2239 GCGCTATCTGCAAGCAATTTGCAAGCAATTTGCAAGCAATTTGCAAGCAATTTGCA 2298
 QY 742 IsoleuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIle 761
 DB 2299 GCGCTATCTGCAAGCAATTTGCAAGCAATTTGCAAGCAATTTGCAAGCAATTTGCA 2358
 QY 762 SerGluIleLeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIle 781
 DB 2359 TCAAAAGCTGCAAGCAATTTGCAAGCAATTTGCAAGCAATTTGCAAGCAATTTGCA 2418
 QY 782 GlyLeuSerThrCysGlnSerThrGluGluGluGluGluGluGluGluGluGluGlu 801
 DB 2419 GCGCTATCTGCAAGCAATTTGCAAGCAATTTGCAAGCAATTTGCAAGCAATTTGCA 2478

QY 802 AspArgValIleuLysArgSerAlaGluLysSerAspProLeuLysProLysLeu 821
 DB 2479 GACCTGTGTCAAAACACAGCTGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2538
 QY 822 ArgPheAspIleCysGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSer 841
 DB 2539 GATTTTATATTAAATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 2598
 QY 842 LysPheCysGlnLysLeuAlaGluMetIleSerGluAlaGluMetCysGlnLys 861
 DB 2599 AATTTTCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2658
 QY 862 MetAsnAspSerMetAspThrSerAsnLysGluLys 874
 DB 2659 ATCAATGATCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2697

RESULT 9

US-09-469-522-34

: Sequence 34, Application US/09469522

: Patent No. US20020151461A1

: GENERAL INFORMATION:

: APPLICANT: Xu, Hong-Ji

: Hu, Shi-Xue

: Benedict, William F.

: Zhou, Yunli

: TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR

: PROTEINS

: NUMBER OF SEQUENCES: 51

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Arnold, White & Burkee

: STREET: P.O. Box 4433

: CITY: Houston

: STATE: TX

: COUNTRY: USA

: ZIP: 77210-4433

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US-09-469,522

: FILING DATE: 22-Dec-1999

: CLASSIFICATION: G06K9/00

: PRIORITY APPLICATION DATA:

: APPLICATION NUMBER: 09/046,459

: FILING DATE: <Unknown>

: ATTORNEY/AGENT INFORMATION:

: NAME: Hubler, David W.

: REGISTRATION NUMBER: 41,071

: REFERENCE/DOCKET NUMBER: UTG:506

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 512/418-3000

: TELEFAX: 512/474-7577

: INFORMATION FOR SEQ ID NO: 34:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 3266 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: Single

: TOPOLOGY: linear

: FEATURE:

: NAME/KEY: CDS

: LOCATION: 7..2502

: SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US-09-469-522-34

Alignment Scores:

Pred. No.: 0 Length: 3266

Score: 4273.00 Matches: 831

Percent Similarity: 100.00% Gaps: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 94.87% Indels: 0

DB: 10 Gaps: 0

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 64 ThrGluLeuGlnLysAsnLeuLeuLeuSerValHisLysPhePheAsnLeuLeuLysGlu 83
 70 AATGAGTAAACAAAAAATAAATAACAGTGGTAAATTAATTAATTAATTAATTAATTAAT 129
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 130 ATTAGAATCAATGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 169
 104 LeuPheAlaLeuPheSerLysLeuGlnAlaThrCysLeuLeuLeuLeuLeuGlnPro 123
 160 TTCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCAT 249
 124 SerSerSerHisSerThrGluHisAsnSerAlaLeuValLeuLysValSerTrpIleThr 143
 250 APTAGTTCATATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 309
 144 PheLeuLeuAlaLysGlyLeuValLeuGluMetGluAspAspLeuValHisSerPheGln 163
 310 TTTTATTAGCTAAAGAGAGATATTAGAAATGGAATGATCTGGTGAATTTGATTTTTCAG 369
 164 LeuMetLeuCysValLeuAspThrPheLeuLysLeuSerProProMetLeuLeuLysGln 183
 370 TTAATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429
 184 ProThrLysThrAlaValIleProHisAsnGlySerProArgThrProAsnArgGlyGln 203
 430 TCAATAAATAAGCTGCTAT 489
 204 AsnArgSerAlaArgIleAlaLysGlnLeuGluAspThrArgIleIleGluValLeu 223
 490 AACAGAGTGCAGGATAGGAAATAGTAAATAGTAAATAGTAAATAGTAAATAGTAAATAG 549
 224 CysLysGlnHisGlnLysAsnLeuAspGluValHisAsnValThrPheCysAsnPheIle 243
 550 TCTAAAGAAATGAAGAAATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 609
 244 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeu 263
 610 CTTTTHAAGAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669
 264 SerLysArgTyrgIleGlnIleThrLysLysAsnLysAspLeuAspAlaArgLeuPheLeu 283
 670 TTAAGGATAAGAAAGAAATTTATCTTAAATAAATGATGATGATGATGATGATGATGAT 729
 284 AspHisAspLysThrLeuGlnIleHisAspSerIleAspSerPheGlnThrGlnArgThrPro 303
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 304 ArgLysSerAsnLeuAspGluValAsnValIleProProHisThrProValArgThr 323
 790 CAAAAAAGTAACTTCACTCAAAAGTCAAAAGTCAAAAGTCAAAAGTCAAAAGTCAAAAG 849
 324 ValMetAsnThrIleGlnIleLeuMetMetIleLeuAsnSerAlaSerAspGlnProSer 343
 850 GTTATGAAATATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 909
 344 GluAsnLeuIleSerThrPheAsnAsnGlyThrValAsnProLysGlnSerIleLeuLys 363
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 384 CysValGlnIleGlySerGlnArgTyrgLysLeuGlyValArgLeuTyrgValMet 403

DB 1030 TGTGTGAAATTTGGATCATACAGGATATAAAATTGCAATTCTGTGTATTAATGAAATATG 1089
 QY 404 GluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeu 423
 DB 1090 GAATGCAATGCTTAAATACAAACAAACAAACATTAACCAATTAATAATTTACAAATTTG 1149
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 DB 1150 AATGCAATCATTTTCTCAATCTCTTATCTGCGTGGCTTTTGAGGTCTGAAAGTGGTACA 1209
 QY 444 TyrSerArgSerThrSerGluAsnLeuAspSerGlyThrAspLeuSerPheProThrPhe 463
 DB 1210 TATGCAAGATATACATCTGCAATCTGATCTGCAATCTGCAATCTGCAATCTGCAATCT 1269
 QY 464 LeuAsnValLeuAsnLeuLysAlaPheAspPheTyrgLysValIleGlnSerPheLeuLys 483
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 QY 504 MetGluSerLeuAlaIlePheLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLys 523
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 QY 564 SerThrThrArgValAsnSerThrAlaAspAlaGlnThrGlnAlaThrSerAlaPheGln 583
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 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
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US 09 469-522-3
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US-09-026-459 522-48

: Sequence 48, Application US/09469522

: Patent No. US20020151461A1

: GENERAL INFORMATION:

: APPLICANT: Xu, Hong-Ji

: Hu, Shi-Xue

: Henedict, William F.

: Zhou, Yunli

: TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR

: NUMBER OF SEQUENCES: 51

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Arnold, White & Durkee

: STREET: P.O. Box 4433

: CITY: Houston

: STATE: TX

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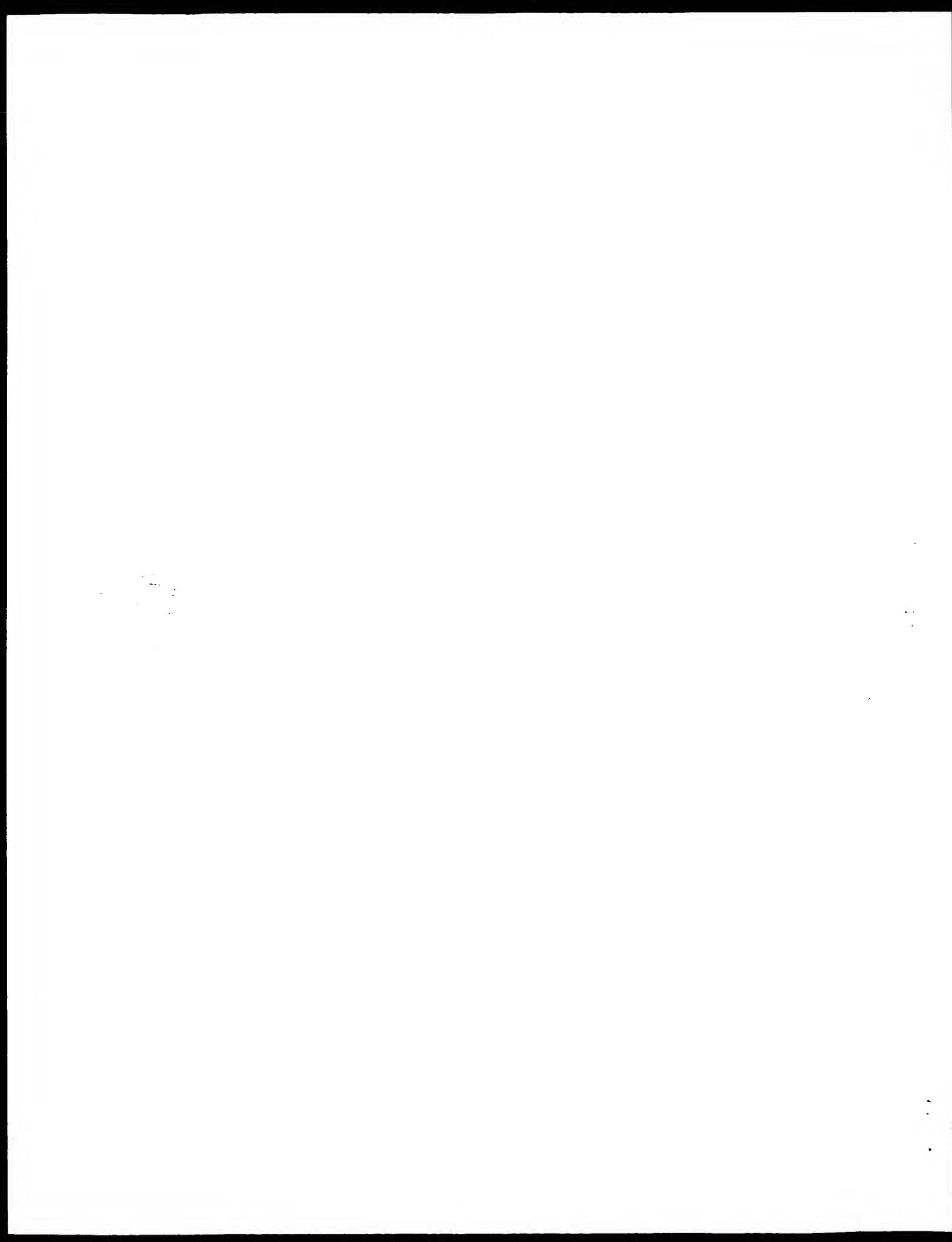
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Genature version 5.1.3
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US-09-026-459A-47: -p2n -db: with -model: frame_p2n.model -db: with

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US-09-026-459A-47: -p2n -db: with -model: frame_p2n.model -db: with

US-09-026-459A-47: -p2n -db: with -model: frame_p2n.model -db: with

US-09-026-459A-47: -p2n -db: with -model: frame_p2n.model -db: with

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Sequence 50, Appl
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Sequence 1153, App
Sequence 186, App
Sequence 163, App
Sequence 136, App
Sequence 2540, App
Sequence 4, Appl
Sequence 305, App
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Sequence 145, App
Sequence 989, App
Sequence 216, App
Sequence 181, App
Sequence 1242, App
Sequence 1, Appl
Sequence 154, App
Sequence 267, App
Sequence 179, App
Sequence 359, App
Sequence 40, Appl
Sequence 279, App

ALIGNMENTS

Sequence 46, Application US-09469522

Patent No. US20020151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-di

Hu, Shi Xue

Henedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED RETINOLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Burke

STREET: P.O. Box 4444

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4444

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US20020151461A1

FILING DATE: 22-Dec-1999

CLASSIFICATION: <UNKNOWN>

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4502	100.0	3371	10	US-09-469-522-46
2	4454.5	98.9	3555	10	US-09-469-522-1
3	4454.5	98.9	4859	9	US-09-464-531-143
4	4444.5	98.7	2995	10	US-09-860-211-7


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1518 GTAAATCAAGAAAGAAAGCAATTATCATTCATAATTTAGCAAACTTCTGAATGACAC 1577
422 TlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArg 441
1578 ATTTTCATATGCTTATTCGCTCGCTCTTCAGGTTCTAATGCCACATATACGAGA 1637
442 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnVal 461
1638 AGTACATCTCAGAAATCTGATTCGCAAGAGATTTGTTCATGATGATGAAATG 1697
462 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGly 481
1698 CTATTTTAAAGAGCTTTGATTTTAAAGAGATGTAAGGTTTATCAAGAGAGAGGC 1757
482 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSer 501
1758 AACTTCACACACAAAGAAAGAAATTTAGAACGATGCAACATCGAATCATGCAATCC 1817
502 LeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGlu 521
1818 CTTCATGGCTCTCAATTAATTAATTTATTTATTTATTAATAAATAAGAGAGAGAA 1877
522 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProGluGlnAsnHis 541
1878 GAGCAACTCATATTAATTAATTTATTTATTTATTTATTTATTTATTTATTTATTT 1947
542 ThrAlaAlaAspMetTyrLeuSerPheValArgSerProLysLysLysSerThr 561
1948 ACTGCACGATATGATATCTTCCTCTGTAAGATCTCCAAAGAAAAAGCTTCAACTAGC 1997
562 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGluThrGlnLys 581
1998 GGTAAATTTATTAAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2057
582 ProGlySerThrSerLeuSerGluPheTyrLysValTyrArgGluAlaTyrLeu 601
2058 GATTAATAATCTAGCTCTTTCCTGTTTATTAATAATAATAATAATAATAATAATAATA 2117
602 ArgLeuAsnThrLeuGlyAlaLeuLeuSerGluHisProGluLeuHisIleIle 621
2118 GGGTAAATTAATTAAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2177
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2178 TGGAGCTTTTCCAGAGAAAGCTGTAAGATGATGAACTATCATCATCATCATCATCAT 2237
642 AspGluHisMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLys 661
2238 GAGCAAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2297
662 PheLysIleIleValThrAlaTyrLeuLysAsnLeuProHisAlaValGluGluThrPheLys 681
2298 TCAAAATCACTTAACACACATACAGAGATCTTCCTGAGCAATCTTCAGAGACATTCAAA 2357
682 ArgValLeuIleLysGluGluGluTyrAspSerIleIleValPheTyrAsnSerValPhe 701
2358 AGTCTTTTATCAAAAGAAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2417
702 MetGluAlaIleLysThrAsnIleGluGlnTyrAlaSerThrArgProTyrGluLeuSer 721
2418 ATGAGAAATGAGAAATAATATTTTATGATGATGATGATGATGATGATGATGATGATG 2477
722 ProIleProHisIleProArgSerProTyrLysPheProSerSerProLeuAlaIlePro 741
2478 GCAATACATCAATCCGCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2537
742 GlyTyrAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGlyLeuPro 761

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Db 2538 GAGGAGAAATATATATTTATGAGGAGAAAGATGATGATGATGATGATGATGATGAT 2597
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QY 782 ThrSerGluLysPheGlnLysIleAspGlnMetValCysAsnSerAspArgValLeuLys 801
Db 2658 ACTTCCTCAACACTTCCAGAAAAATAATACAGATGAGTAATCAACAGACGACGCTGCT 2717
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QY 842 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetLysAspSerMet 861
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QY 862 AspThrSerAsnLysGluGlyLys 869
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RESULT 4
US-09-860-211-7
: Sequence 7, Application US/09860211
: Patent No. US-600,493,721,2A1
: GENERAL INFORMATION:
: APPLICANT: Gregory, Richard J.
: Inventor: Willis, Ken N.
: TITLE OF INVENTION: Recombinant Adenoviral Vector and
: METHOD OF USE
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESS: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/860,211
: FILING DATE: 18-May-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/328,673
: FILING DATE: 15-FEB-2000
: APPLICATION NUMBER: US 08/142,669
: FILING DATE: 25-OCT-1993
: APPLICATION NUMBER: US 08/233,669
: FILING DATE: 26-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, Timothy S.
: REGISTRATION NUMBER: 35,367
: REFERENCE/DOCUMENT NUMBER: 016930 00092005
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2995 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear

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RESULT 7
US-69-469-522-40
Sequence 40, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: XU, Hong Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOLASIOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4434
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4434
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PatcEdit Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 69-469-522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 69-026-459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 01XC-506

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RESULT 7
US-69-469-522-40
Sequence 40, Application US/09469522
Patent No. US20020151461A1
GENERAL INFORMATION:
APPLICANT: XU, Hong Ji
Hu, Shi-Xue
Benedict, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINOLASIOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: P.O. Box 4434
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4434
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PatcEdit Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 69-469-522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 69-026-459
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 01XC-506

357 LeuTysArgValTysAspTleGlyTyrIlePheCysGlyTysPheAlaLysAlaValGly 376
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477 IleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHis 496
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497 ArgIleMetGluSerLeuAlaIlePheSerAspSerProLeuPheAspLeuIleLysGln 516
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1750 TCCAGAGCCAGAGGCAATGAAATCTACCTCTCTTTCACCTCTCTTTTATTAATAAGTGTAT 1809
597 ArgLeuAlaTyrLeuArgLeuAsnThrLeuGlyGluArgLeuLeuSerGluHisProGlu 616
1810 GGGTATGCTATCTGAGGTAATAATATTTTGAGAAATTTTGTGTGAGTATGCAAA 1869
617 LeuGluHisIleIleThrPheLeuPheGlnHisThrLeuGluAsnGluTyrGluLeuMet 636
1870 TACACATATCACTGCCACCCCTTTCACACACACCCCTCCACAAACAGATCACTCAATC 1929
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1930 ACACAGGCTATTTGCAAAATATGATGTGTCTTCCATCTATGCAATATGCAATATGCAAG 1989
657 AspIleAspLeuLysPheLysIleLeuValThrAlaTyrLysAspLeuProThrIleAlaVal 676
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697 TyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGluTyrAlaSerThrArg 716
2110 TATAAGTGTGTCTTATGAGAGAGCTGAAAGCAAAATTTTGTAGTATGCTTCCAGAGG 2169

717 ProGluLeuSerProIleProHisIleProAlaGlySerProTyrLysPheProSer 736
2170 GGGCTATCTTTCATATAATATTTAAATATTTAAATATTTAAATATTTAAATATTT 2229
737 ProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIle 756
2230 GGTACAGGATCTTCAGAGCAACATATATTTCAACCTTCAACCTTCAACCTTCAACCTT 2289
757 SerGluGlyLeuProThrProThrIysMetThrProArgSerArgIleLeuValSerIle 776
2290 TGAAGAGTCTTCACACCAACCAAAATGCTCCAAATCANGAATCTTATATCAAT 2349
777 GlyGluSerPheGlyThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSer 796
2350 GGTGAATATTGAGAAATTTTASAGATTCAGAAATATTAATCAGATGATGATGATGATGAT 2409
797 AspArgValLeuLysArgSerAlaGluGlySerAsnProProLysProLeuLysLysLeu 816
2410 GACCTGTCTCTCAAGAGAGTCTCAAGAGCAACCTCTCTCAACCTCTCAACCTCTCAACCT 2469
817 ArgPheAspIleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSer 836
2470 GGTGTGATATTAAATATTTAAATATTTAAATATTTAAATATTTAAATATTTAAATATTT 2529
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2530 AATTTTCAGTAAATATTTAAATATTTAAATATTTAAATATTTAAATATTTAAATATTT 2589
857 MetAsnAspSerMetAspThrSerAsnLysGluGluLys 869
2590 ATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2628

RESULT 10

US-09-469,520-42

Sequence 42, Application US/09/469522

Patent No. US2002015161A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

Hu, Shi-Xue

Benedict, William F.

Zhou, Yunli

TITLE OF INVENTION: MODIFIED KETINOLASINOMY TOMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/469,522

FILING DATE: 22-Dec-1999

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/469,459

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41-071

REFERENCE/DOCKET NUMBER: UTXC:506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 3347 base pairs

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97	61	CysGluLysLeuLysIleProAspHisValArgGluAlaIrpLeuThrTrpGluLys	80
100	96	-----	96
99	81	ValSerSerValAspCysValLeuGlyGlyTyrLeuGluTyrLysGluLeuTrpCys	100
100	96	-----	96
99	101	IleCysIlePheIleAlaValAspLeuAspGluMetSerPheThrPheThrGluLeu	120
100	97	-----GTCACCCACAGACATGCTGCTACCTTATCTGAGACTA	135
99	121	GluLysAsnIleGluIleSerValHisLysPheAsnLeuLeuLysGluIleAspThr	140
100	136	CAGAAAAATAGAAATCAGTGTCAATAAATCTTTAACTTACTAAGAAATGATACC	195
99	141	SerThrLysValAspAsnAlaMetSerArgGluGluLeuLysTyrAspValLeuPheAla	160
100	196	ATATACAAATTTGATATATTTATTTAAATATTTGAAATATATTTATTTTATTTT	255
99	161	LeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGluProSerSerSer	180
100	256	CTCTTCAGCAAAATTCGAAAGACAAATGTGAATCTATATATTCACACACCCACCTTCG	315
99	181	Met-----	181
100	316	ATATCTATGAAATGAAATTCCTGCTATGCTGCTGCTAAAAGTTCTTGGATCACATTTTATTA	375
99	181	-----	181
100	376	GCTAAAGGAGAGTATTACAAATGCAAGATGATCTGCTGCTATTCTATTTCAGTTAAATGCTA	435
99	181	-----	181
100	436	TGTCGCTTGACATATTTATTAAGCTTCACCTTCCTGCTGCTGCTCAAGAACCATATAAA	495
99	182	ValAlaValIleProIleAsnGlySerProArgThrProArgAspArgGluAsnArgSer	201
100	496	ACAGCTGTTATACCAATTAAATGTTACCTCAAAATACCAAGTCAGCTACAAAGAT	555
99	202	AlaThrLeuAlaLysGluLeuLeuLysAspPheAlaIleCysValLeuGlySerGlu	221
100	556	GACGCTATGCAAAACATACAAATATGATATTAAGATTTGAAATCTGCTGTAAGAA	615
99	222	HisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnProIleProPheMet	241
100	616	TAAGAAATGAATATAGACAGGTCAGAAATGTTATTTCAAAATTTATACCTTTTATG	675
99	242	AsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArg	261
100	676	AAATCTTTGCACTTGTATATATATATGATATTCACAGATGTGAAGAAATCTTGTATAAACA	735
99	262	TyrGluGluIleTyrLeuLysAsnLysAspIcuAspAlaArgLeuPheLeuAspHisAsp	281
100	736	TACAGAAATATTTATCTTAAATAAAGATCTAGATGCAATATTTTGGATCAIGAT	795
99	282	LysThrLeuGluThrThrAspSerIleAspSerPheGluThrGluInArgThrProArgLysSer	301
100	796	AAAACCTCTTCACATGATCTCTATACAGCTTTGAAACACACAGAACACCCAGAAAAGCT	855
99	302	AsnLeuAspGluGluValAsnValIleProProHisThrProValArgThrValMetAsn	321
100	856	AAATTTGAGAGAGAGTCAATGTAATTCCTCTCACACATCAATGATGAGATGTTAAGAA	915
99	322	ThrIleGluGluGluMetMetIleGluAsnSerAlaSerAspGluProSerGluAsnLeu	341
100	916	ATATGCAACAATTAATGATGATTTTAAATTCAGCAAGTGTCAACCTTCAGAAAATCTG	975

Q7	342	IleSerThrPheAsnAspGluSerThrValAsnGluLeuSerIleLeuLeuLysArgValLys	361
DB	976	ATTTGCTATTTTAAACAAGTCGACAGTCAAATCCAAAAGAAAGATACGCAAAAGAGACGAAAG	1045
QY	362	AspIleGlyTyrIlePheThrGlySerGluThrPheGluAlaValIleGluGlyGlySerValGlu	381
DB	1036	GATATAGGATACATTTTAAAGAGAATTTGTAAAGTGTGTGGAGAGGGGTGTGTGAA	1095
QY	382	IleGlySerGlnArgTyrTyrGlySerGluGlyValArgGluSerTyrTyrAlaValMetGluSerMet	401
DB	1096	ATTGCAATCACAGTCATACAACATTGGAGATGGGTTTGATATCCGAGTAAATGCAATCCATG	1155
QY	402	IleTyrSerGluGluGlyArgGluSerIleGlnAsnPheSerLysPheLeuAsnValAsn	421
DB	1136	CTTAATATCAGAAGAGAACCATTAATCAATCAAAATTTTAGCAAACTTTGCAATCATCAAC	1215
QY	432	IleIleHisMetSerIleGluAlaCysAlaLeuGlyValIleMetAlaLeuThrTyrSerArg	441
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QY	442	SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTyrPheLeuAsnVal	461
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QY	462	LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGly	481
DB	1336	CTTAATTTAAAGCGCTTGATTTTACAAAGTGAATCCAAAGTTTATCAAGACGACAAAGC	1395
QY	482	AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSer	501
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DB	1636	CGTGCTAAATTCATCTGAAAATAGACACAAAGCAAGGTCAGGCTTCCAGCCGACGAAG	1695
QY	582	ProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeu	601
DB	1696	CGATTGAATCACTCTCTTCCACGTCTTATAAAAAAGTGTATCGCTACGCCATATCTC	1755
QY	602	ArgLeuAsnSerThrLeuGlyGluArgGluLeuSerGluHisIleGluLeuHisIleGlu	621
DB	1756	CGGTATTAATATACCTTGTGAAGAGGCTCTGTCTGACACACCAAAATAGAAATATATATAT	1815
QY	622	TyrThrLeuThrGluHisThrIleGluGlnAsnGlyTyrGluLeuMetArgAspArgHisIleu	641
DB	1816	TGCACTTTTTCAGGCACACACCTTCAGAAATGAGTATCAACATCATGAGACAGACGACATTC	1875
QY	642	AspGlnLeuMetIleGlySerMetIleGlyIleGlyGluValLysAsnIleAspLeuArg	661
DB	1876	GACCAAAATATGATGCTTCCATGCTATGCCATATGCCAAAGTCAGAAATACACCTTAAA	1935
QY	662	PheGlyIleLeuAlaThrAlaTyrLysAspLeuThrHisAlaValGlnIleuThrPheLys	681
DB	1936	TTCAAAATCATGTAAATAGATATATAAAGATCTGATGATGATGATGATGATGATGATGATGAT	1995
QY	682	ArgValIleuLeuLysGluThrPheThrAspSerIleGluValPheTyrAsnSerValPhe	701
DB	1996	CGCTGTTTTGATCAAGAGAGGAGGATGATGATCTATATAGTATTTCTATATACCTGGCTCTC	2055
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674  HisAlaValGlnGlnThrPheLysArgValLeuIleIleLysGluGluGluTyrAspSerIle 693
1867  CATGGCTGTCAGAGAAATTCGAATGTTTTCATTAAGAGAGAGAGATGATGATTTTAT 1926
694  IleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAla 713
1927  ATAGTATTCATTAACATCGCTTCATCGACACACTCAAAACAAAATATTTTCACATAGCT 1986
714  SerThrArgProThrLeuSerProIleProIleProIleProIleProIleProIleProIle 733
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2107  TATAAATTCACAGAGGCTCTGCAATCAACCAACCAAAATCACATCCCAAGATCAAGAAATCTTA 2166
774  ValSerIleGlyGluSerPheGlyThrSerGlyLysPheGlnLysIleAsnGlnMetVal 793
2167  GTATCAATTTGTTAAATATTGAGGAAATTTCTTAAAGATTCGACAAAATATATATATATAT 2226
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2287  AAAAAATATGCTTTCATATATCAACATCATCAGATGAGGAGAGATGGAAGTAAACATCTGCA 2346
834  ThrGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThrArgThrArgMetGln 853
2347  GATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 2406
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Search completed: January 19, 2003, 05:46:21
 Job time: 156.436 secs

Database version 5.1.4
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CM protein nucleotide search, using frame_plus.p2n model
P2N ID: January 18, 2003, 04:31:54 : Search type: 1, seqs: 3
(without alignments)
6107.852 Million cell updates/sec

Filter: US 09 026 459A 49

Percent score: 44.96

Sequence: 1 MPRKPRKIAIAAAAAEP.....IMOKRMNDISNKKEK 871

Scoring tables: BLOSUM62

Xgapop 10.0 : Xgapext 0.5

Ygapop 10.0 : Ygapext 0.5

Fgapop 6.0 : Fgapext 7.0

Delop 6.0 : Delext 7.0

Searches: 43868 seqs, 22294149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listed first 45 summaries

Command line parameters:

MODEL frame.p2n model DEV.xlh

DB-published Applications NA -GEMT-fastap -SUFFIX-rnpb -MINMATCH-0.1

TRANS human40.cdb -L180-45 -LOCAL-ON-200 -THR SCORP-pet -THR MAX-100

THR MIN-0 -ALIGN 15 -MODE-LOCAL -OUTFMT-pet -NORM-ext -HEAPSIZE-500 -MINLEN-0

MAXLEN-2000000000 USER-DS002459-seqN-1-1-500 -format-160120083-152189-23469

NTP 6 -1000 5 -N XLPXY -NO MAP -LARGEQUERY -NEG SCORES-0 WAIT -LONGHUG

DEV TIMEOUT 120 WARN TIMEOUT 40 -THREADS 1 XGAPOP-10 XGAPEXT-0.5 -FCGAPOP-6

F-GAPEXT 7 YGAPOP-10 YGAPEXT-0.5 DELOP-6 -DELEXT-7

List those :

Published Applications_NA:

Seq	Score	Match	Length	ID	Description
1	44.96	100.0	43868	10	US 09 469 522-48
2	44.47	98.7	4555	10	US 09 469 522-40
3	44.47	98.7	4555	10	US 09 469 522-40
4	44.47	98.7	4555	10	US 09 469 522-40
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45	44.47	98.7	4555	10	US 09 469 522-40

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	44.96	100.0	43868	10	US 09 469 522-48
2	44.47	98.7	4555	10	US 09 469 522-40
3	44.47	98.7	4555	10	US 09 469 522-40
4	44.47	98.7	4555	10	US 09 469 522-40

ALIGNMENTS

RESULT 1

US-09-469 522-48
Sequence 48: Application: US/09445522
Patent No. US5520151461A1

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Benedit, William E.
Zhou, Yun-Ji

TITLE OF INVENTION: MODIFIED PEPTIDE-BLASTOMA TUMOR SUPPRESSOR

PROTEINS

NUMBER OF SEQUENCES: 51

SUPPLEMENTARY ACCESS:

ADDRESSEE: Arnold, White & Burke

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-09-469 522

FILING DATE: 22 Dec 1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09-026-459

FILING DATE: UNKNOWN

ATTORNEY/AGENT INFORMATION:

NAME: HIBERT, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: UTX-506

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-1000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 3383 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURES:

NAME/KEY: CDS

LOCATION: 7..2619

SEQUENCE DESCRIPTION: SEQ ID NO: 48

US-09-026-459

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Db 2898 GATAGCTCAAAACAGGAGAGAGAA 2921
RESULT 4
US-09-026-211-7
: Sequence 7, Application US/09860211
: Patent No. US20020197211A1
: GENERAL INFORMATION:
: APPLICANT: Greiner, Richard J.
: Willis, Ken N.
: Maneval, Daniel C.
: TITLE OF INVENTION: Recombinant Adenoviral Vector and
: METHODS OF USE
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Townsend and Townsend and Crew LLP
: STREET: TWO Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.10
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/860,211
: FILING DATE: 18 May 2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/328,673
: FILING DATE: 15-FEB-2000
: APPLICATION NUMBER: US 08/142,669
: FILING DATE: 25-OCT-1993
: APPLICATION NUMBER: US 08/243,669
: FILING DATE: 26-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, Timothy S.
: REGISTRATION NUMBER: 35,367
: REFERENCE NUMBER: 01433-000200S
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2495 base pairs
: TYPE: nucleic acid
: STRAIN: single
: TOPOLOGY: linear

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16 1940 AATTAAAGCTGTTTATGAAAGAGGATGATGATCTATATAGTATCTATAAG 1989
17 201 GATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
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32 880 14
33 78 09 469 522 4
34 Sequence A, Application US/09469522
35 Patent No. US2002013461A1
36 GENERAL INFORMATION:
37 APPLICANT: Xu, Hong-shi
38 Hu, Shi-xue
39 Benedict, William F.
40 Zhou, Yunli
41 TITLE OF INVENTION: MODIFIED RETIN/BLASTOMA TUMOR SUPPRESSOR
42 PROTEINS
43 NUMBER OF SEQUENCES: 51
44 CORRESPONDENCE ADDRESS:
45 ADDRESSEE: Arnold, White & Burkee
46 STREET: P.O. Box 4433
47 CITY: Houston
48 STATE: TX
49 COUNTRY: USA
50 ZIP: 77210 4433
51 COMPUTER READABLE FORM:
52 MEDIUM TYPE: Floppy disk
53 COMPUTER: IBM PC compatible
54 OPERATING SYSTEM: PC DOS/MS-DOS
55 SOFTWARE: Patent to Release #1.0, Version #1.40
56 CURRENT APPLICATION DATA:
57 APPLICATION NUMBER: US/09469,522
58 FILING DATE: 22-Dec-1999
59 CLASSIFICATION: Unknown
60 PRIOR APPLICATION DATA:
61 APPLICATION NUMBER: 09/026,459
62 FILING DATE: Unknown
63 ATTORNEY/AGENT INFORMATION:
64 NAME: Hubler, David W.
65 REGISTRATION NUMBER: 41,071

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REFERENCE/KEY: CDS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-4000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4218 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 7..2454
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-469-522-3
Alignment Scores:
Pred. No.: 0 Length: 4218
Score: 4842.50 Matches: 759
Percent Similarity: 94.01% Conservative: 0
Best Local Similarity: 94.01% Mismatches: 0
Query Match: 85.46% Indels: 57
Gaps: 2
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RESULT 15
US-09-469-522-44
Sequence 44, Application US/09469522
Patent No. US20040151461A1
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
Hu, Shi-Xue
Hendrick, William F.
Zhou, Yunli
TITLE OF INVENTION: MODIFIED RETINGBLASTOMA TUMOR SUPPRESSOR
PROTEINS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Burke
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER PHASABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY NAME: US 2004 469 522
FILING DATE: 22-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,459
 FILING DATE: UNKNOWN
 ATTORNEY/AGENT INFORMATION:
 NAME: HELLER, David W.
 REGISTRATION NUMBER: 41-071
 REFERENCE/DOCKET NUMBER: UTXC:506
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-4000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3141 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..2397
 SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Alignment Scores:		
Prod. No.:	0	Length: 3161
Score:	3799.00	Matches: 755
Percent Similarity:	87.21%	Conservative: 28
Best Local Similarity:	96.19%	Mismatches: 9
Query Match:	84.50%	Indels: 94
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14 2110 CTATCAATGCTGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2169
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14 2290 GGCAGAGTCAAAATTCAGCAGCAAAATTCAGCAGCAAAATTCAGCAGCAAAATTCAGCAGCAAA 2349
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Search completed: January 19, 2003, 05:47:54
Job time : 156.582 secs

Sequence 4, Application US/9801092
 Patent No. 6074959
 GENERAL INFORMATION:
 APPLICANT: Autolman, Douglas
 APPLICANT: Gregory, Richard J.
 APPLICANT: Wells, Kenneth N.
 TITLE OF INVENTION: Tissue Specific Expression of
 TITLE OF INVENTION: Retinoblastoma Protein
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: CA

COUNTRY: USA
 ZIP: 94111
 COMPUTER AVAILABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/9801092
 FILING DATE: 14 FEB 1997
 CLASSIFICATION: 514

PREVIOUS APPLICATION DATA:
 APPLICATION NUMBER: US 08/751 517
 FILING DATE: 15 NOV 1996
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Ellis, Pease A.
 REGISTRATION NUMBER: 35,146
 REFERENCE/DOCKET INFORMATION: 016930-001020
 TELEPHONE/DOCKET INFORMATION:
 TELEPHONE: 415-576-0200
 TELEFAX: 704-576-0400
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2994 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQ ID NO: 4

Alignment Scores:
 Prod. No.: 2994
 Score: 4609.00
 Matches: 894
 Percent Similarity: 100.00%
 Conserved: 0
 Best Local Similarity: 100.00%
 Mismatches: 0
 Gaps: 0
 Quality: 99.80%
 Indels: 0
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 10 461 TGTATTAATTTGAC 420
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QY 702 ValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 721
DB 2341 GTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
QY 722 PheTyrAsnSerValPheMetGluArgIleIleIleIleIleIleIleIleIleIleIleIle 741
DB 2401 TTTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
QY 742 ArgProIleThrLeuSerProIleProIleIleProIleProIleProIleProIleProIle 761
DB 2461 AAAAAAGGTCAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
QY 762 SerProLeuArgIleProIleGlyAsnIleIleIleIleIleIleIleIleIleIleIleIle 781
DB 2521 TCAATTTAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
QY 782 HisSerGluGlyLeuProIleProIleProIleProIleProIleProIleProIleProIle 801
DB 2581 ATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2640
QY 802 IleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 821
DB 2641 ATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700

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QY 822 SerAspArgValIleuIysArgIleIleIleIleIleIleIleIleIleIleIleIleIle 841
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QY 842 LeuArgPheAspIleGlySerAspGluAlaAspGlySerIysHisLeuProIleGlu 861
DB 2761 CTACCTTTCAATATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
QY 862 SerIysPheIleGlyLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIle 881
DB 2821 TCCAAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
QY 882 IysMetAsnAspSerMetAspThrSerAsnIysGluIleIys 895
DB 2881 AAAATGATATATATATATATATATATATATATATATATATATATATATATATATATAT 2922

RESULT 4
US-09-315-113-3
: Sequence 3, Application US/09315113
: Patent No. 6379927
: GENERAL INFORMATION:
: APPLICANT: Antelman, Douglas
: Gregory, Richard J.
: Wills, Kenneth N.
: TITLE OF INVENTION: Tissue Specific Expression of
: Retinoblastoma Protein
: NUMBER OF SEQUENCES: 46
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/315,113
: FILING DATE: 19-May-1999
: CLASSIFICATION: <unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/801,092
: FILING DATE: <unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitts, Renee A.
: REGISTRATION NUMBER: 35,136
: REFERENCE/WORKIT NUMBER: 616330 603020
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-576-0200
: TELEFAX: 703-576-0300
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2994 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-315-113-3

Alignment Scores:
Pred. No.: 0 Length: 2994
Score: 4609.00 Matches: 894
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 4 Gaps: 0
US-09-026-459a-29 (1-895) x US-09-315-113-3 (1-2994)

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100 56  ProGlySerProSerProGluArgIleProGlyGlyAsnIleThrIleSerPro 775
101 114  CATTAAAGTTTCTAGTTCATGCTTACGATTCGAGAGAACATATATATTTTACCT 1131
102 176  LeuGlySerProSerProGlyGlyLeuProThrProThrLeuMetThrProArg 795
103 113  CTAAGACAGTCAATATAAAATTCACAGCTTCGACACCAACCAACAAATGATCCAGA 1071
104 206  SerAlaIleLeuValSerIleGlyGlySerProThrProGlyGlyProGlyGly 815
105 207  TCAAAAGATCAGTAAATGAGGAAATGATGAGAAATTTCTAGAGGATGAGAAATA 1011
106 816  AsnGluMetValGlyAsnSerAspArgValIleLeuSerSerAlaGlyGlySerPro 835
107 101  AATCAGATGATGATGAAAGAGAGATGTTGTCAAAAGATGCTGAGGAGAAAGCT 951
108 836  ProGlyProLeuGlyGlySerLeuArgProGlyGlySerAspGlyGlyGlySer 855
109 837  CCAAAATACCAAAATACGATTCATGATTCAGAGATGACATGACAGCAGATGGAAT 891
110 838  LysIleLeuProGlyGlySerProGlyGlyGlySerProGlyGlyGlySerPro 875
111 839  AAATATCTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 831
112 840  ThrArgMetGlnGlyGlyGlyMetAspSerMetAspThrSerAsnGlyGlyGly 895
113 841  ACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771

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RESULT 10

US-09-026-459a-29.rni

Sequence 1: Application US/08470091

Patent No. 5912236

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

INVENTOR: Xu, Hong-Ji

ADDRESS: Beijing, China

TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and

METHODS FOR Tumor Suppressor Gene Therapy.

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER: IBM PC compatible

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

APPLICANT'S DATA:

APPLICATION NUMBER: US/08470091

FILING DATE: JUN-16-1995

CLASSIFICATION: 514

FROM APPLICATION DATA:

FILING DATE: JUN-16-1995

FILING DATE: JUN-16-1995

ATTORNEY/AGENT INFORMATION:

NAME: Pennie & Edmonds

FEDERATION NUMBER: 28,462

REFERENCE/WORK NUMBER: 7404 025 994

TELEPHONE INFORMATION:

TELEPHONE: (212) 760-6090

TELEFAX: (212) 869 9741/8864

TELETYPE: (212) 760-6090

INFORMATION FOR SMO TO NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4242 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

REMARKS: not relevant

MOLECULE TYPE: DNA

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FEATURES:
NAME/KEY: CDS
LOCATION: 19...2469
US-08-470-091.1
Alignment Scores:
Pred. No.: 0
Length: 3232
Score: 4213.00
Matches: 820
Percent Similarity: 100.00%
Mismatch: 0
Query Match: 91.31%
Indels: 0
Gaps: 2
US-09-026-459a-29 (1-995) x US-08-470-091 (1-3232)

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QY 76  AspLeuAspGluMetSerPheThrPheThrGluLeuGluLysAsnIleLeuSerVal 45
DB 7  GACCTAGATCAGATGCGGTTCACCTTTACGACCTACACAGAAACATACAAATACGTC 66
QY 96  HisIysPhePheAsnIleLeuValLeuAspThrSerThrIysValAspAsnAlaMet 115
DB 67  CATAAATCTTTAACTTACTTAAAGAAATGATACAGTACAGTACCAAAATGATTAATG 126
QY 116  SerArgIleuLeuIysIysIysIysValLeuPheAlaLeuPheSerIysIysIysIys 135
DB 127  TCAACAGCTGTGAAGAAATATGATGATGATGATGATGATGATGATGATGATGATG 186
QY 136  CysGluLeuIleThrLeuThrGlnProSerSerSerIleSerThrGluLeuLeuSerAla 155
DB 187  GTCGCAATATATATATATATATATATATATATATATATATATATATATATATATAT 246
QY 156  LeuValIleuIysValSerThrIleThrPheLeuLeuAlaIysGlyGlyValIleuLeuMet 175
DB 247  TTGCTGCTAAAGATTTCTTGATGATCAATTTTATTTAGTAAAGGGGAGATATTATTA 306
QY 176  GluAspIleuValIleSerPheGlnLeuMetLeuCysValLeuAspIysIysIysIys 195
DB 307  GACATGATCTGGTGAATTCATTTCAATTAATGATGATGATGATGATGATGATGATG 366
QY 196  LeuSerProProMetLeuLeuLysGluProThrLysThrAlaValIleProGlyLeuGly 215
DB 367  CTTCTACCTCCCTATGTTGCTTCAAGAGCACTAATAAACACCTGTTATACCATTAAT 426
QY 216  SerProArgThrProArgGlyGlnAsnArgSerAlaArgIleAlaIysIysIysIys 235
DB 427  TCACTCTGAAATATGAGAGATATATATATATATATATATATATATATATATATAT 486
QY 236  AspAspThrArgIleGlyGlyValIleGlyGlySerIleSerIleSerIleSerIle 255
DB 487  AATGATACAGAAATATTGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 546
QY 256  LysAsnValIysPheLysAspPheIleProIleMetAspSerLeuGlyLeuValThr 275
DB 547  AAAAAATGTTTATTCAAAAATTTTATACCTTTTATCAATTTCTCTCTCTCTCTCTCT 606
QY 276  AspGlyIleProGlyGlyValIleGlyGlySerIysValIleGlyGlyGlyGlySer 295
DB 607  AATGCACTTTCAGAGTTGAAATCTTTTAAAGTATGATGATGATGATGATGATGATG 666
QY 296  LysAspLeuAspAlaIleIlePheIleAspPheIleAspPheIleAspPheIle 315
DB 667  AAACATCTACATCAAGATATTTTGGATCAGTAAACATCTCTCTCTCTCTCTCTCTCT 726
QY 316  AspSerPheIleThrIleArgThrProArgIysSerAsnIleAspGluIleValAsnVal 335
DB 727  GACACTTTTCAACATACAGAGAACACCAACCAACCAACCAACCAACCAACCAACCA 786
QY 336  IleProIleIleProValArgThrValMetAspThrIleGlnIleLeuMetThr 355
DB 787  ATTCCTCCACACATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 846
QY 356  LeuAsnSerAlaSerAspIleProSerGluAsnIleIleSerIlePheAsnAspThr 375
DB 846  TTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 932

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[illegible][illegible]

